(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
8 April 2004 (08.04.2004)

PCT

(10) International Publication Number
WO 2004/028346 A2

(51) International Patent Classification[7]: A61B

(21) International Application Number:
PCT/US2003/030359

(22) International Filing Date:
25 September 2003 (25.09.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/413,583 25 September 2002 (25.09.2002) US
60/491,842 1 August 2003 (01.08.2003) US

(71) Applicant *(for all designated States except US)*: **AMERSHAM BIOSCIENCES (SV) CORP.** [US/US]; 928 East Arques Avenue, Sunnyvale, CA 94085 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **LOUKOLA, Anu-Maria** [FI/FI]; Mäkitie 4, FIN-02880 Veikkola (FI). **PENN, Sharron, Gaynor** [GB/US]; 1529 School Street, San Carlos, CA 94070 (US). **RANK, David, Russell** [US/US]; 886 Bruce Drive, Palo Alto, CA 94303 (US). **HANZEL, David, Kagen** [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). **CASEY, Graham** [GB/US]; 55 Skyline Drive, Moreland Hills, OH 44022 (US). **WITTE, John, S.** [US/US]; 2931 Frontera Way, Burlingame, CA 94010 (US).

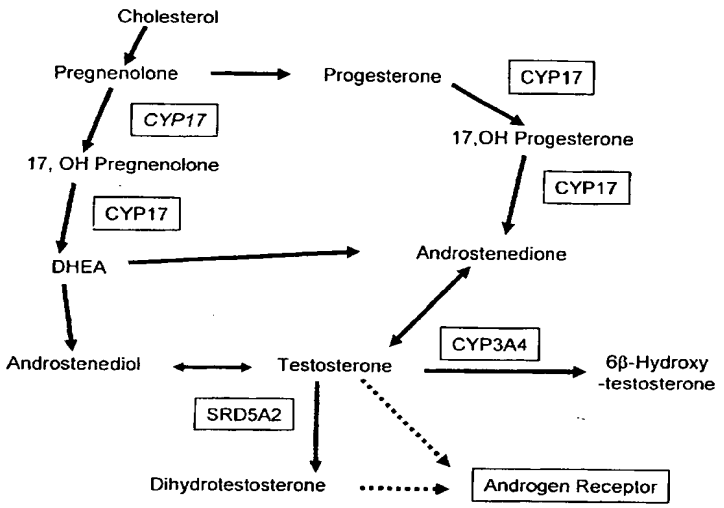
(74) Agents: **JI, Yonggang** et al.; Amersham Biosciences Corp, 800 Centennial Avenue, Piscataway, NJ 08855 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: DETECTION METHODS



Testosterone biosynthetic pathway

(57) Abstract: The present invention relates to the prognosis, diagnosis and treatment of cancer, particularly prostate cancer. Polynucleotides having single nucleotide polymorphisms (SNPs) and haplotypes are provided which are of utility in the prognosis, diagnosis, prophylaxis and treatment of prostate and breast cancer.

WO 2004/028346 A2

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

DETECTION METHODS

Cross Reference to Related Applications

This application claims priority to United States provisional patent application numbers 60/413,583 filed September 25, 2002, and 60/491,842 filed August 1, 2003; the disclosures of which are incorporated herein by reference in their entirety.

Field of Invention

The present invention relates to single nucleotide polymorphisms in nucleic acids involved in encoding enzymes in the testosterone biosynthetic pathway and to methods for detecting such polymorphisms. The invention has utility in the diagnosis, prognosis, prevention and treatment of disease, particularly those relating to prostate cancer and breast cancer.

Background of the Invention

Prostate cancer is the most common non-skin cancer in males all over the world. Currently, there are no means to predict how aggressive an individual's cancer will be. Thus, many patients are given unnecessary drastic treatment with severe side effects and possibly others do not receive treatment effective enough.

Incidence of prostate cancer shows strong age dependence, being a disease of old men, and strong race dependence, being almost twice as common in African Americans as in Caucasians, while Asian populations have the lowest risk (Cook et al. (1999) J Urol 161, 152-155; Hsing et al. (2000) Int J Cancer 85, 60-67). The third well-known risk factor is having a family history of prostate cancer (Cerhan et al.(1999) Cancer Epidemiol Biomarkers Prev 8, 53-60; Kalish et al. (2000) Urology 56, 803-806), and several studies have supported the presence of predisposing genetic factors.

Genome wide linkage analyses have pointed multiple chromosomal regions showing linkage in prostate cancer families and several prostate cancer candidate loci have been suggested; HPC1 in 1q24 (Smith et al. (1996) Science 274, 1371-1374), HPCX in Xq27 (Xu et al. (1998) Nat Genet 20, 175-179), PCAP

in 1q42.2 (Berthon et al. (1998) Am J Hum Genet 62, 1416-1424), CABP in 1p36 (Gibbs et al. (1999) Am J Hum Gen 64, 776-787), and *HPC2/ELAC2* in 17p (Tavtigian et al. (2001) Nat Genet 27, 172-180). Recently, a candidate cancer-susceptibility gene, *RNASEL*, was cloned at the HPC1 loci (Carpten et al. (2002) Nat Genet 30, 181-184) and two possibly deleterious germline mutations segregating in prostate cancer families were discovered.

The growth of prostate cells is dependent on active testosterone (Ekman (1995) J Urol 101, 22-25) and strikingly, prostate adenocarcinomas can be created by testosterone administration in rats (Gupta et al. (1999) Cancer Res 59, 2115-2120). Testosterone seems to be a strong tumour promoter for the rat prostate, even at doses that do not measurably increase circulating testosterone (Bosland et al. (1991) Princess Takamatsu Symp 22, 109-123). Consequently, genes involved in the testosterone biosynthetic pathway, e.g., *CYP17*, *CYP3A4*, and *SRD5A2* (Figure 1) are good candidates for being involved in the initiation and progression of prostate cancer. Several polymorphisms have been discovered in these genes and some of them show association either with increased risk or progression of prostate cancer (Table 1). Nevertheless, there is no evidence of higher testosterone levels in prostate cancer patients.

Approximately 55 different Cytochrome P450 genes are present in the human genome and are classified into different families and subfamilies on the basis of sequence homology. Members of the CYP3A subfamily catalyze the oxidative, peroxidative and reductive metabolism of different endobiotics, drugs, and protoxic or procarcinogenic molecules. As an example, CYP3A4 is responsible for the oxidative metabolism of an estimated 60% of all clinically used drugs. Up to 30-fold interindividual differences in expression has been detected, causing variation in oral bioavailability and systemic clearance of CYP3A substrates, such as HIV protease inhibitors, several calcium channel blockers and some cholesterol-lowering drugs. Variation in CYP3A expression is particularly important in substrates with narrow therapeutic indices, such as cancer chemotherapeutics and immunosuppressants. Variation in CYP3A expression can result in clinically significant differences in drug toxicities and response.

As with prostate cancer, breast cancer also shows age-dependency indicating a possible hormonal influence on the disease risk. Endogenous oestradiol synthesis takes place in the ovarian theca cells of pre-menopausal women, in the stromal adipose cells of the breast of post-menopausal women, and in minor quantities in peripheral tissue. These cells, as well as breast cancer tissue, express all the necessary enzymes for this synthesis, including *CYP17*, and enzymes that further hydroxylate oestradiol, such as *CYP3A4* (Kristensen et al. (2000) Mutat Res 462, 323-333). Thus, polymorphisms in these enzymes may also be associated with the risk of breast cancer (Kristensen et al. (2000) Mutat Res 462, 323-333). Furthermore, *CYP3A4* is also involved in the activation of many mammary carcinogens, such as the polycyclic aromatic hydrocarbons and heterocyclic amines (Guengerich et al. (1991) Chem Res Toxicol. 4, 168-179). According to a recent study (Zheng et al. (2001) Cancer Epidemiol Biomarkers Prev 10, 237-242), high *CYP3A4* activity may be a risk factor for breast cancer risk.

Single nucleotide polymorphisms (SNPs) are the most common type of genetic variation in the human genome, and are expected to be helpful in identifying human disease genes. In addition to occurring frequently, on average every 500-2,000 bp (Li & Sadler (1991) Genetics 129, 513-523; Chakravarti (1998) Nat Genet 19, 216-217; Cargill et al. (1999) Nat Genet 22, 231-238; Halushka et al. (1999) Nat Genet 22, 239-247), SNPs have a low mutation rate when compared to microsatellite markers, both of which are characteristics that may have particular advantages for association analysis. The utility of SNPs is not only in their use as markers for discovering additional functional variants and for the general evaluation of a specific gene in the context of a given clinical phenotype but also in their potential functional relevance. However, rather than finding a single SNP with drastic effect on the phenotype, more likely it will be multiple SNPs in relevant genes, either linked (i.e., grouped as a haplotype) or independent (perhaps on different chromosomes), that contribute to the phenotype.

Recently, several studies have shown the utility of haplotypes, i.e., a combination of SNPs with alleles physically assigned to a chromosome, in association analysis (Daly et al. (2001) Nat Genet 29, 229-232). Studying

haplotypes might give the analysis more power but traditionally demands either samples from multiple generations or tedious molecular haplotyping. Alternatively, several algorithms have been developed for inferring haplotypes from genotype data (Clark (1990) Mol Biol Evol 7, 111-122; Excoffier & Slatkin (1995) Mol Biol Evol 12, 921-927; Stephens et al. (2001) Am J Hum Genet 68, 978-989). These algorithms have been proven to work with a very low error rate (Drysdale et al. (2000) PNAS 97, 10483-10488). In a sense, haplotyping is equivalent to performing a study in a family or other select group of people. It helps to get back the power of linkage, and can be regarded as a crucial step in association studies using random individuals.

WO02/055735 discloses specific nucleic acids useful for identifying, diagnosing, monitoring, staging, imaging and treating prostate cancer and breast cancer. Similar compositions comprising prostate specific nucleic acids are described by the same applicant (Diadexus Inc.) in related applications (WO02/42776, WO02/42499, WO02/42463, WO02/42329, WO02/39431, WO02/239431, WO02/38810, WO02/38810, WO02/236808 and WO0224718).

Diadexus Inc. have also disclosed a method of diagnosing, monitoring, staging, imaging and treating prostate and breast cancer by means of specific nucleic acids, in a series of related applications (WO01/39798 & WO00/23111 & WO00/23108).

WO01/53537 (DZ Genes Inc.) describes isolated polynucleotides containing at least one polymorphism useful for the diagnosis of disease, particularly prostate and breast cancer.

Single nucleotide polymorphisms associated with prostate cancer are disclosed in WO01/83828, as are methods for using these SNPs to determine susceptibility to this disease.

In order to improve the lives of prostate and breast cancer patients it is essential to develop prognostic markers for cancer as well as markers allowing general assessment of disease risk. Patients need to be categorized into those needing immediate, extensive treatment, and those who just need watchful waiting. As a result, prostate and breast cancer mortality could be reduced and unnecessary side effects caused by invasive treatments could be avoided. There is therefore a need for prognostic molecular markers for aggressive breast and

prostate cancer to aid predicting, diagnosing and monitoring these diseases in individuals. Furthermore, there is a continued need for improved methods of treatment of both conditions in patients. The present invention addresses these needs and provides improvements over the prior art in the form of novel and specific nucleic acids, microarrays and kits useful for the diagnosis of breast and prostate cancer.

Summary of the Invention

According to the first aspect of the present invention, there is provided an isolated polynucleotide selected from the group consisting of a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS 1-34. Suitably, a fragment of the isolated polynucleotide comprises a polymorphic site in the polymorphic sequence.

In a second aspect of the present invention, there is provided an isolated polynucleotide comprising a sequence complementary to one or more of the polymorphic sequences of SEQ ID NOS 1-34. Suitably, a fragment of the complementary nucleotide sequence comprises a polymorphic site in the polymorphic sequence.

Preferably, the polynucleotides of the first and second aspect comprise DNA, RNA, cDNA, or mRNA

Preferably, at least one single nucleotide polymorphism of the isolated polynucleotide is at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15,

position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, and position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34.

More preferably, at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1

+466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, and [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34.

Optionally, the polynucleotide is the complement of any of the isolated polynucleotides hereinbefore described.

In one aspect, the polynucleotide comprises part of the *CYP17* gene, the *CYP3A4* gene or the *SRD5A2* gene.

Preferably, the isolated polynucleotide further comprises a detectable label. More preferably, the detectable label is selected from the group consisting of fluorophore, radionuclide, peptide, enzyme, antibody and antigen. In a preferred embodiment, the fluorophore is a fluorescent compound selected from the group consisting of Hoechst 33342, Cy2, Cy3, Cy5, CypHer, coumarin, FITC, DAPI, Alexa 633, DRAQ5 and Alexa 488.

In a third aspect of the present invention, there is provided a method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, the method comprising analysing a biological sample containing nucleic acid obtained from the subject to detect the presence or absence of one or more single nucleotide polymorphisms at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of

SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44, and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

Suitably, the nucleic acid is DNA, RNA, cDNA or mRNA.

Preferably, the single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19,

[CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No.45.

Optionally, the single nucleotide polymorphism is selected from the complement of any of the single nucleotide polymorphisms described hereinbefore.

Suitably, the analysis is accomplished by sequencing, genotyping, fragment analysis, hybridisation, restriction fragment analysis, oligonucleotide ligation or allele specific PCR. Preferably, the analysis is accomplished by hybridisation, the method comprising the steps of

i) contacting the nucleic acid with an oligonucleotide that hybridises to one or more isolated polynucleotide polymorphic sequence selected from the group consisting of SEQ ID NOS 1-36, 42-45 or its complement

ii) determining whether the nucleic acid and the oligonucleotide hybridize;

whereby hybridisation of the nucleic acid to the oligonucleotide indicates the presence of the polymorphic site in the nucleic acid.

In a fourth aspect of the present invention, there is provided a method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, or predicting an individual's response to a

drug, the method comprising adding an antibody to a polypeptide present in a biological sample obtained from the subject which polypeptide is encoded by a polynucleotide selected from the group consisting of SEQ ID NOS 1-36 and SEQ ID NOS 42-45, or the complement thereof, and detecting specific binding of the antibody to the polypeptide.

In a fifth aspect of the present invention, there is provided a kit comprising at least one isolated polynucleotide of at least 5 contiguous nucleotides of SEQ ID NOS: 1-36 or 42-45, or the complement thereof, and containing at least one single nucleotide polymorphic site associated with a disease, condition or disorder related to prostate or breast cancer together with instructions for the use thereof for detecting the presence or the absence of said at least single nucleotide polymorphism in said nucleic acid.

In a sixth aspect of the present invention, there is provided an oligonucleotide array comprising at least one oligonucleotide capable of hybridising to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide comprises a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS: 1-36 and SEQ ID NOS: 42-45.

Suitably, the first polynucleotide comprises a fragment of any of the nucleotide sequences, the fragment comprising a polymorphic site in the polymorphic sequence.

Suitably, the first polynucleotide is a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences of SEQ ID NOS: 1-36 and SEQ ID NOS: 42-45.

Suitably, the first polynucleotide comprises a fragment of said complementary sequence, the fragment comprising a polymorphic site in the polymorphic sequence.

Suitably, the position of the polymorphic site in the kit or the microarray as hereinbefore described is at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -

132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34.position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

Preferably, at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after

the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

Optionally, at least one single nucleotide polymorphism is the complement of any of the single nucleotide polymorphisms as hereinbefore described.

Suitably, the oligonucleotide further comprises a detectable label. Preferably, the label is selected from the group consisting of fluorophore, radionuclide, peptide, enzyme, antibody or antigen. More preferably, the fluorophore is a fluorescent compound selected from the group consisting of Hoechst 33342, Cy2, Cy3, Cy5, CypHer, coumarin, FITC, DAPI, Alexa 633 DRAQ5 and Alexa 488.

In a seventh aspect of the present invention, there is provided a method of treatment or prophylaxis of a subject comprising the steps of

i) analysing a biological sample containing nucleic acid obtained from the subject to detect the presence or absence of at least one single

nucleotide polymorphism in SEQ ID NOS 1-36 or SEQ ID NOS 42-45, or the complement thereof, associated with a disease, condition or disorder related to prostate or breast cancer; and

ii) treating the subject for the disease, condition or disorder if step i) detects the presence of at least one single nucleotide polymorphism in SEQ ID NOS: 1-36 or SEQ ID NOS 42-45, or the complement thereof.

Treatment may take a variety of forms depending upon the nature of the cancer. Hormonal therapy is a widely used treatment for patients with metastatic carcinoma of the prostate (Goethuys et al. (1997) Am J Clin Oncol. 20, 40-45). Such treatment may, for example, involve androgen deprivation by surgical (e.g. orchiectomy) or androgen suppressive agents such as estrogens, (e.g.diethylstilbestrol), antiandrogens (e.g. flutamide) and luteinising hormone-releasing hormone agonists (e.g. leuprolide). Radiotherapy using radionuclides, such as ^{32}Phosphorus or ^{89}Strontium, can be an effective treatment for the disease. There is also growing interest in the development of vaccines (Slovin (2001) Hematol. Oncol. Clinic N. Am, 15, 477-496) or the use of gene therapeutic methods (Ferrer & Rodriguez (2001) Hematol Oncol Clinic of N. Am 15, 497-508) for the treatment of prostate cancer.

Suitably, the nucleic acid is selected from the group consisting of DNA, RNA and mRNA.

Preferably, the sample is analysed to detect the presence or absence of at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position

[CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34.position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44, and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

More preferably, at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17,

[CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

Optionally, at least one single nucleotide polymorphism is the complement of any of the single nucleotide polymorphisms hereinbefore described.

Suitably, the method counteracts the effect of at least one single nucleotide polymorphism detected.

In a first embodiment of the seventh aspect, the method comprises treatment with a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS 1-36 or SEQ ID NOS 42-45, or their complement, provided that the polymorphic sequence, or the complement, does not contain at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon,] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon,] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base

pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44, and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

Preferably, the polymorphic sequence does not contain at least one single nucleotide polymorphism selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13,

[CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

Preferably, the polymorphic sequence does not contain at least one single nucleotide polymorphism which is the complement of any of the single nucleotide polymorphisms hereinbefore described.

In a second embodiment of the seventh aspect, the method comprises treatment with a polypeptide which is encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS 1-36 and SEQ ID NOS 42-45 or their complement, provided that the polymorphic sequence, or the complement, does not contain at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ

ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

Preferably, the polymorphic sequence does not contain at least one single nucleotide polymorphism selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3

+1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36,[CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

Suitably, the polymorphic sequence does not contain at least one single nucleotide which is the complement of any of the single nucleotide polymorphisms as hereinbefore described.

In a third embodiment of the seventh aspect, the method comprises treatment with an antibody that binds specifically with a polypeptide encoded by a polynucleotide selected from the group consisting of SEQ ID NOS 1-34, or SEQ ID NOS 42-45, or the complement thereof.

According to an eighth aspect of the present invention, there is provided a method for predicting the genetic ability of a subject or an organism to metabolise a chemical, the method comprising analysing a biological sample containing nucleic acid obtained from the subject or organism to detect the presence or absence of one or more single nucleotide polymorphisms at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2,

position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44, and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

Wherein the presence of a polymorphism at one or more of the positions is indicative of the subject's or organism's ability or inability to metabolise the chemical.

Preferably, the analysis comprises detecting the presence or absence of one or more single nucleotide polymorphisms selected from the group consisting

of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

Preferably, the method further comprises predicting the response of the subject or the organism to the chemical by their ability or inability to metabolise the chemical.

Suitably, the chemical is a drug or a xenobiotic.

Suitably, the organism is selected from the group consisting of bacterium, fungus, protozoa, alga, insect, nematode, amphibian, plant, fish and mammal.

In a ninth aspect of the present invention, there is provided a vector comprising a polynucleotide selected from the group consisting of a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS 1-34 or SEQ ID NOS 42-45.

In a tenth aspect of the present invention, there is provided a host cell transformed with the vector hereinbefore described.

Preferably, the host cell is selected from the group consisting of, bacterium, fungus, protozoa, alga, insect, nematode, amphibian, plant, fish and mammal. More preferably the mammalian cell is a human cell.

In an eleventh aspect of the present invention, there is provided a method of metabolising a chemical using the host cell as hereinbefore described.

In a twelfth aspect of the present invention, there is provided a method for making a host cell resistant to a chemical, the method comprising transforming a cell with any of the polynucleotides or with any of the vectors as hereinbefore described.

In a thirteenth aspect of the present invention, there is provided an isolated haplotype selected from the group consisting of CYP3A4_Hap4 and SRD52_Hap3.

Preferably, the isolated CYP3A4_Hap4 haplotype consists of Allele T at [CYP3A4_5' region –1232C>T], Allele C at [CYP3A4_5' region –747C>G], Allele G at [CYP3A4_5' region –392A>G], Allele G at [CYP3A4_IVS7+34T>G], Allele T at [CYP3A4_IVS7-202C>T], Allele G at [CYP3A4_stop+766T>G], Allele C at [CYP3A4_stop+1454C>T], Allele T at [CYP3A4_stop+1639A>T] and Allele C at [CYP3A4_stop+2204G>C].

Preferably, the isolated SRD52_Hap3 haplotype consists of Allele C at [SRD5A2_5' region –8029C>T], Allele G at [SRD5A2_5' region –3001G>A], Allele G at [SRD5A2_145G>A], Allele G at [SRD5A2_265G>C], Allele T at [SRD5A2_IVS2+626C>T], Allele G at [SRD5A2_stop+1552G>A], Allele G at [SRD5A2_stop+3059G>A] and Allele G at [SRD5A2_stop+9301G>C].

In a fourteenth aspect of the present invention, there is provided a method for diagnosing a genetic susceptibility for a disease, condition or disorder related

to prostate or breast cancer in a subject, the method comprising analysing a biological sample obtained from the subject to detect the presence or absence of a haplotype as hereinbefore described.

In a fifteenth aspect of the present invention, there is provided a method of diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, the method comprising adding an antibody to a polypeptide present in a sample obtained from the subject, which polypeptide is encoded by a haplotype as hereinbefore described, or the complement thereof, and detecting specific binding of the antibody to the polypeptide.

In a sixteenth aspect of the present invention, there is provided a method of treatment or prophylaxis of a subject comprising the steps of

i) analysing a sample of biological material containing a nucleic acid obtained from the subject to detect the presence or absence of at least one haplotype as hereinbefore described, or the complement thereof, associated with a disease, condition or disorder related to prostate or breast cancer; and

ii) treating the subject for the disease, condition or disorder if step i) detects the presence of at least one haplotype, or the complement thereof.

Preferably, the method comprises treatment with a portion of the isolated CYP3A4_Hap4 haplotype as hereinbefore described wherein the portion of the haplotype does not consist of at least one allele from the group consisting of Allele T at [CYP3A4_5' region –1232C>T], Allele C at [CYP3A4_5' region –747C>G], Allele G at [CYP3A4_5' region –392A>G], Allele G at [CYP3A4_IVS7+34T>G], Allele T at [CYP3A4_IVS7-202C>T], Allele G at [CYP3A4_stop+766T>G], Allele C at [CYP3A4_stop+1454C>T], Allele T at [CYP3A4_stop+1639A>T] and Allele C at [CYP3A4_stop+2204G>C].

Optionally, the method comprises treatment with a portion of the the isolated SRD5A2_Hap3 haplotype as hereinbefore described wherein the portion of the haplotype does not comprise of at least one allele from the group consisting of Allele C at [SRD5A2_5' region –8029C>T], Allele G at [SRD5A2_5' region –3001G>A], Allele G at [SRD5A2_145G>A], Allele G at [SRD5A2_265G>C], Allele T at [SRD5A2_IVS2+626C>T], Allele G at

[SRD5A2_stop+1552G>A], Allele G at [SRD5A2_stop+3059G>A] and Allele G at [SRD5A2_stop+9301G>C].

Brief Description of the Figures

Figure 1 illustrates the Testosterone Biosynthetic Pathway.

Figures 2A, 2B, and 2C show the location and allele frequencies of selected SNPs in *CYP17A1* (FIG. 2A), *CYP3A4* (FIG. 2B), and *SRD5A2* (FIG. 2C), together with the major haplotypes. Solid black triangles refer to the locations of novel SNPs while white triangles denote locations of known SNPs. All haplotypes with frequency ≥3% in at least one of the four sub-groups (European Americans(EA), African Americans(AA), cases, controls) are given, along with their case and control frequencies. Composite haplotype refers to all the remaining rare haplotypes pooled together.

Detailed Description of the Invention

Approach

A two-phase study was undertaken of CYP17, CYP3A4, and SRD5A2, to evaluate the relationship between their genotypes/haplotypes and prostate cancer. Phase I of the study first searched for single nucleotide polymorphisms (SNPs) in these genes by re-sequencing 24 individuals from Coriell Polymorphism Discovery Resource (Coriell Cell Repositories, Camden, NJ), approximately 100 men from prostate cancer case-control sibships, and by leveraging public databases. Eighty-seven SNPs were discovered and genotyped in 276 men from case-control sibships. Those SNPs exhibiting preliminary case-control allele frequency differences, or distinguishing (i.e., 'tagging') common haplotypes across the genes, were identified for further study (24 SNPs total). In Phase II of the study, the 24 SNPs were genotyped in an additional 841 men from case-control sibships. Finally, associations between genotypes/haplotypes in CYP17, CYP3A4, and SRD5A2 and prostate cancer were evaluated in the total case-control sample of 1,117 brothers.

Subjects

A family-based association study population of 1,117 men (637 cases, 480 controls) was recruited between January 1998 and January 2001 from the major medical institutions in the greater Cleveland area and from the Henry Ford Health System in Detroit. The study was approved by the collaborating institution's Review Boards, and informed consent was obtained from all participating men. Characteristics of the study population have been described (Casey et al. (2002) Nat Genet 32, 581-583).

Men diagnosed with histologically confirmed prostate cancer at age 73 or younger were invited to join the study if they had a living unaffected brother who was either older than the proband, or at most eight years younger than the age at diagnosis of the proband. This age restriction was selected in an attempt to increase the potential for genetic factors affecting disease, and to help make certain that the controls were not unaffected due simply to being of a younger age. To help confirm that the controls were not diseased, theprostate specific antigen (PSA) levels in their blood was tested. Individuals in the study with PSA levels above 4 ng/ml were retained as 'controls' unless a subsequent diagnosis of prostate cancer was made, at which time they were reclassified as cases. Keeping them in the study was important because automatically excluding men with elevated PSA levels regardless of their ultimate prostate cancer status can lead to biased estimates of association (Lubin & Hartge (1984) Am J Epidemiol 120, 791-793; Poole (1999) Am J Epidemiol 150, 547-551). Information on the cases' Gleason score (a measure of prostate cancer cellular differentiation) and tumor stage (TNM, tumor-node-metastasis stage) was determined from their medical records. The study population was comprised of 90% Caucasians (European Americans), and the remainder primarily African American (9%).

Polymorphism discovery

Polymorphisms were discovered by sequencing individuals from prostate cancer sibships (67 cases and 43 controls for CYP17 and CYP3A4, and 51 cases and 41 controls for SRD5A2). Of the 110 individuals sequenced for CYP17 and CYP3A4, 106 were Caucasian, 2 were Hispanic, and 2 were African-American. Of the 92 individuals sequenced for SRD5A2, 84 were Caucasian and 8 were

African American. In addition, the 24 individuals from the Coriell Cell Repository Polymorphism Discovery Resource (Collins et al. (1998) Genome Res 8, 1229-1231) were sequenced against the three genes.

PCR primers covering coding regions, splice sites, 5' and 3' regions, and parts of introns of *CYP3A4* (reference sequence No. 39), *CYP17* (reference sequence No. 40), and *SRD5A2* (reference sequence No. 41), were designed using the Primer3 program (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi). PCR products were sequenced using energy transfer dye terminators on the Amersham Bioscience's MegaBACE1000 (Amersham Biosciences, Sunnyvale, California) using standard protocols. Sequence analysis was performed by assigning quality values (Phred; University of Washington, Seattle, Washington), assembling contigs (Phrap; University of Washington), automated identification of candidate heterozygote SNPs (PolyPhred, University of Washington), automated identification of candidate homozygote SNPs (High Quality Mismatch, Amersham Biosciences, Sunnyvale, California) and by operator confirmation (Consed, University of Washington). All polymorphisms were confirmed by Single Nucleotide Primer Extension (SNuPE) assay (Amersham Biosciences, Sunnyvale, California)

In addition to novel polymorphisms discovered in this study, several publicly available SNPs from the dbSNP (http://www.ncbi.nlm.nih.gov/SNP/), Utah Genome Center (UGC) (http://www.genome.utah.edu/genesnps/genes/), the Human Cytochrome P450 Allele Nomenclature Committee (HCANC) (http://www.imm.ki.se/CYPalleles/), the Human Gene Mutation Database (HGMD) (http://archive.uwcm.ac.uk/uwcm/mg/hgmd0.html) and the Human Genic Bi-Allelic SEquences (HGBASE) Release 8 (http://hgbase.interactiva.de/) were searched for *CYP17*, *CYP3A4*, and *SRD5A2*. For the *Androgen Receptor* gene, several publicly available SNPs from dbSNP, HGBASE and the Androgen Receptor Mutation Database (ARMD) (http://ww2.mcgill.ca/androgendb/) were included.

Genotyping

In Phase I, 276 individuals from prostate cancer sibships were genotyped for 29 SNPs (11 novel, 18 known) in *CYP17*, 33 SNPs (18 novel, 15 known) in

CYP3A4, and 25 SNPs (5 novel, 20 known) in *SRD5A2*. The individuals included 153 cases and 123 brother controls, 70% European Americans and 30% African Americans. The information from the 276 men was then used to determine initial case-control frequency differences and haplotype tagging. The results were then used to determine which SNPs should be genotyped in the remainder of the study population (i.e. in Phase II of the study).

In Phase II, a total of 24 SNPs were genotyped in 841 individuals, giving information on a total of 1117 individuals for Phase II .

Genotyping was performed utilizing the Single Nucleotide Primer Extension (SNuPE) assay on the MegaBACE1000 (Amersham Biosciences, Sunnyvale California) capillary electrophoresis platform (Amersham Biosciences). The Primer3 program (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi) was used to design PCR primers to amplify regions containing the SNPs of interest.. PCR fragments were purified with 0.5U of Shrimp Alkaline Phosphatase (Amersham Biosciences) and 10U of Exonuclease I (Amersham Biosciences) by incubating at 37°C for 40 min and at 85°C for 15 min. The single base extension (SBE) reaction was set with 1 pmol of HPLC purified SBE primer, 2-4 μl of SNuPe Premix (Amersham Biosciences), 2-4 μl of sterile water, and 1 μl of purified PCR fragment, and incubated at 25 cycles of 96°C for 10 sec, 50°C for 5 sec, and 60°C for 10 sec. For phase I of the study, SNuPe reactions were set in 96-well plates at 10 μl volume and purified with AutoSeq^{TM}96 Plates (Amersham Biosciences) prior to injecting into the MegaBACE1000 system. For phase II of the study, SNuPe reactions were set in 384-well plates at 5-6 μl volume, diluted with 3-4 μl of sterile water and purified with 1 U of Shrimp Alkaline Phosphatase (Amersham Biosciences) by incubating at 37°C for 45 min and at 85°C for 15 min prior to injecting into the MegaBACE4000 system. In cases where low signal was anticipated (due to faint PCR), SNuPe reactions were desalted using a custom 384-well filter plate incorporating modified size-exclusion technology (Millipore Corporation, Billerica, MA). The Scierra Genotyping LWS^{TM} (Amersham Biosciences) system was utilized for the tracking and management of samples and laboratory activity for Phase II of the study.

Specific software (SNPriDe) was developed for the automated design of SNuPE primers. Using a purified PCR fragment containing the SNP of interest as

a template, a third, internal primer was designed so that the 3' end anneals adjacent to the polymorphic base-pair, and during the SNuPE reaction a fluorescently labeled dideoxynucleotide (terminator) was added onto the primer. A separate software package has been developed (SNP Profiler™, Amersham Biociences) that automatically processes the signal data and outputs the maximum likelihood SNP genotypes. The system includes a user interface for editing and verification.

Three SNPs, SRD5A2_SNP20 (V89L), SRD5A2_SNP22 (A49T) and CYP17-_SNP29(-34>C) were analysed by restriction enzyme digestion (Cicek et al., unpublished data).

Proofreading genotype data

A large number of haplotypes inferred during initial rounds of haplotyping implied erroneous genotype data. A phylogenetic study of inferred haplotypes was performed to reveal the relationships between different haplotypes. All haplotypes differing from another haplotype by only one SNP, and being represented by only one individual, were subject to inspection. Genotype data for the individual at stake were reanalysed by SNP Profiler™ (Amersham Biosciences) to exclude the possibility of an incorrect genotype. Rounds of phylogenetic study of haplotypes, followed by reanalysing suspicious genotypes and inferring new haplotypes were applied until no more incorrect genotypes could be found. Three to six rounds were applied for each of the genes.

Haplotyping

Alleles within each of the three candidate genes were in strong linkage disequilibrium with one another. Thus, for each gene, haplotypes were estimated using the resulting genotypes, by disease status and within major ethnic groups using the software PHASE. This program uses Markov chain Monte Carlo to estimate haplotypes, imputes information for missing genotypes, and incorporates a statistical model for the distribution of unresolved haplotypes based on coalescent theory (Stephens et al. (2001) Am J Hum Genet 68, 978-989).

Haplotypes and haplotype tagging SNPs were first determined among the 276 men genotyped for Phase I of the study, where tagging SNPs was necessary to define the most common haplotypes (e.g., >5%). After completing genotyping on the entire study population (Phase II of the study), the resulting data were used to estimate haplotypes.

Association analysis

Case versus control allele frequencies were first compared within major ethnic groups. Then the association between the resulting genotypes/haplotypes and prostate cancer risk was evaluated by calculating odds ratios (OR, estimates of relative risk) and 95% confidence intervals from conditional logistic regression with family as the matching variable, using a robust variance estimator that incorporates familial correlations. This is a standard approach for analyzing sibling matched case-control data, although sibling sets without any controls do not contribute any information (197 cases total here) (Breslow and Day (1980) IARC Sci Publ 32, 335-338). In the analyses of CYP17, CYP3A4, and SRD5A2 a log-additive coding was used which treats the most common polymorphism (or haplotype) as the null-risk referent group and assumes that the relative risk of carrying one polymorphism (or haplotype) is the square-root of the risk of carrying two. Since haplotypes were estimated for these three genes, the probabilities of observed haplotypes were used in the analyses (Schaid et al. (2002) Am J Hum Genet 70, 425-434).

To control for potential confounding, age was adjusted for in all regression models. In addition to looking at the main effects of each SNP or haplotype, the analyses were also stratified by the case's disease aggressiveness, where high aggressiveness was defined by TNM stage $\geq$ T2B or Gleason score $\geq$ 7; and low aggressiveness by TNM stage < T2B and Gleason score < 7. All statistical analyses were undertaken with the S+ software (version 6.0, Insightful Corp, 2001).

Polymorphism discovery (Phase I)

A total of 34 novel SNPs were detected: 11 in *CYP17*, 18 in *CYP3A4*, and 5 in *SRD5A2* (Table 2). In addition, 11 SNPs were "rediscovered" from the public

databases. Including these 11 SNPs, 53 SNPs were selected in total from the databases: 18 in *CYP17*, 15 in *CYP3A4*, and 20 in *SRD5A2*. These were chosen based on the intention to obtain an even distribution of SNPs across the genes and the availability in the databases at that time (January-April 2001). Twenty-one SNPs were chosen from dbSNP, 27 from GeneSNPs, 12 from HGMD, 8 from HGVbase, and 2 from HCANC (the total number of SNPs listed here exceeds 53 as several SNPs were present in multiple databases). Table 3 lists all 87 SNPs (34 novel, 53 from databases), with their origins, exact locations and allele frequencies.

Among the 34 novel SNPs, 26 (76%) were discovered in both the Coriell and case-control populations. Three SNPs were only observed in the Coriell data, and the remaining five were found only in the prostate cancer sibships. Of these five, three were relatively rare (allele frequencies 0.2-1.5%), suggesting that they may not have been discovered in the Coriell population simply due to its small sample size (n=24). Nevertheless, the other two SNPs that were only found in the prostate cancer sibships (CYP3A4_SNP12 and CYP17_SNP42) showed higher allele frequencies (7.5% and 21.8%, respectively), suggesting that they might be specific to the prostate cancer case-control population.

Genotypying and Haplotyping

Phase I

The 87 SNPs were geneotyped in a total of 276 males from prostate cancer sibships (29 in *CYP17*, 33 in *CYP3A4*, and 25 in *SRD5A2*). Eleven SNPs gave ambiguous genotyping results. This might have been due to unoptimized genotyping reactions or primer self-priming due to secondary structures and unspecificity of PCR and/or SNuPe primers, especially within the Cytochrome P450 gene family. Of the remaining 76 SNPs, a similar percentage of those novel (41%, or 12/29) and known (38%, or 18/47) had allele frequencies ≥10%. However, 19/47 (40%) of the known SNPs were found to be monoallelic in the 276 men, suggesting that they are either extremely rare, population specific, or artifacts.

In light of these results, the 11 SNPs with ambiguous genotype results, the 19 SNPs that appeared monoallelic in all samples tested, and an additional four

that were seen only in the Coriell Diversity Set but not in the prostate cancer sibships were excluded. Also excluded was one SNP because >15% of data was missing (due to a low success rate for PCR and SNuPe reaction). Finally, 12 SNPs were excluded because their minor allele frequencies were less than 5% in all of the following four subgroups: European Americans, African Americans, cases, and controls (Table 3). Following these exclusions, a total of 40 SNPs remained for consideration in the Phase II association study (14 in *CYP17,* 16 in *CYP3A4*, and 10 in *SRD5A2*) (Table 3).

Using the preliminary genotype information, haplotypes estimated with a frequency ≥5% in at least one of the four major subgroups (i.e., European American, African American, cases, or controls) were identified. Each gene had a single "common" haplotype, with a frequency ranging between 42 and 51 percent (not shown). Haplotype tagging SNPs were identified and used as a basis for inclusion in Phase II of the study. In addition, non-tagging SNPs exhibiting suggestive case versus control allele frequencies were considered (Table 3). Altogether 24 SNPs were selected for Phase II.

Phase II

The 24 tagging and suggestive SNPs were genotyped in an additional 841 men, giving information on a total of 1117 individuals for Phase II. Case versus control allele frequency differences by ethnic group are presented in Table 3. Haplotypes estimated with a frequency ≥3% in at least one of the four major subgroups of the study population were identified. The major haplotypes for *CYP17, CYP3A4,* and *SRD5A2* along with their frequencies are presented in Figure 2.

Association analyses

In the association analyses, no associations between CYP17 genotypes/haplotypes and prostate cancer were detected. When looking at CYP3A4, SNP1 was found to be associated with an approximately 50% reduction in risk (OR=0.53, 95% CI=0.29-0.99; p-value=0.05) (Table 4A). Furthermore, the haplotype analysis revealed an association with an approximately 55% decrease in prostate cancer risk and CYP3A4_Hap4 (OR=0.46, 95% CI=0.21-1.02; p-

value=0.05) (Table 5A). Two SNPs in SRD5A2 were also found to be associated with an approximately 50% increase in prostate cancer risk: SRD5A2_SNP26 (OR=1.57, 95% CI=1.08-2.30; p-value=0.02), and SRD5A2_SNP20 (V89L) (OR=1.56, 95% CI=1.08-2.25; p-value=0.02) (Table 4A). These SNPs, however, were in almost complete linkage disequilibrium.

When the study population was stratified by high and low aggressiveness of prostate cancer, several interesting associations emerged (see Table 4B and 5B). First, five SNPs in CYP3A4 showed statistically significant associations with low aggressiveness: CYP3A4_SNP11 (CYP3A4*1B) (OR=0.20, 95% CI=0.06-0.67; p-value=0.009), CYP3A4_SNP47 (OR=0.19, 95% CI=0.06-0.62; p-value=0.006), CYP3A4_SNP1 (OR=0.21, 95% CI=0.05-0.86; p-value=0.03), CYP3A4_SNP25 (OR=6.54, 95% CI=0.99-43.10; p-value=0.05) and CYP3A4_SNP15 (OR=0.41, 95% CI=0.22-0.79; p-value=0.007). Second, an association was observed between CYP3A4_Hap4 and low aggressiveness (OR=0.06, 95% CI=0.008-0.50; p-value=0.009) (Table 5B). Finally, an inverse association was observed between SRD5A2_Hap3 and high aggressiveness (OR=0.52, 95% CI=0.29-0.91; p-value=0.02) (Table 5B).

Table 6 provides annotation of *CYP3A4*, *CYP17* and *SRD5A2* genomic sequences.

All of the SNPs disclosed in the present invention have utility in the prognosis and diagnosis of prostate and breast cancer.

Although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims. All documents cited herein are incorporated herein by reference in their entirety.

Table 1. Known polymorphisms in *CYP17*, *CYP3A4*, and *SRD5A2* associated with increased risk for prostate cancer or increased risk for progression of prostate cancer.

Gene	Polymorphism	Association with	References
CYP17	-34 bp T→C	increased risk	Lunn et al. (1999) Carcinogenetics 20, 1727-1731 Wadelius et al. (1999) Pharmacogenetics 9, 635-639 Gsur et al. (2000) International Journal of Cancer 87, 434-437 Habuchi et al. (2000) Cancer Res 60, 5710-5713 Kittles et al. (2001) Cancer Epidemiol Biomarkers Prev 10, 943-947
CYP3A4	-392 bp A→G	increased risk, progression	Rebbeck et al. (1998) J Nat Cancer Inst 90, 1225-1229 Paris et al. (1999) Cancer Epidemiol Biomarkers Prev 8, 901-905
SRD5A2	145G>A (A49T)	increased risk, progression	Makridakis et al. (1999) Lancet 354, 975-978 Jaffe et al. (2000) Cancer Res 60, 1626-1630
SRD5A2	265G>C (V89L)	increased risk, progression	Nam et al. (2001) Urology 57, 199-204

Table 2(a) : Novel SNPs

SNP identified in Seq ID Number	Novel SNPs	Location	Comment	Sequence
1	CYP3A4_SNP2	Intron 9 [IVS9 +187C>G]		ATGAGAATTTCTGCCACATAGCAGAACGACACATGTT TGAATGTTATAAGTGGTAGTTGGAGGCACTTTCTAGA GGCATGCAGGCATAGATAGCCATGTT(C/G)TAAGAGT AAAGGGCAACCCTAAGCAAACCTGGCATGCTAGAAA GTCAGTCTGCGGTCTGTGGATCACCTACATCAGATCA AATGCCAATTCTCAGCCTCC
2	CYP3A4_SNP5	1639 base pairs after the stop codon, A>T	Possible association (OR 0.51, 95% CI 0.26-0.99, p=0.05) with prostate cancer in the European American population	TGATAGAAGCCAGGCTTCTCACCTTTGCAGAAGGGA GTCATGGATTCAGAAAGGGAGAAAACTAGCATGAATC CTATGAAATTAGATTGGAATGGATGTA(A/T)CCGTGTA TATTCATACCCTTGTAGATAGATAGATGGGTAGATAG ATGATAGATAGGTAACAGATAGATGACAGATAATGAG ATAGATAGATGTAAATGTA
3	CYP3A4_SNP6	945 base pairs after the stop codon, A>T		GGCAGGAGAATCACTTGAACCTGGGAGGCGGATGTT GAAGTGAGCTGAGATTGCACCACTGCACTCCAGTCT GGGTGAGAGTGAGACTCAGTCTTAAAAA(A/T)ATATGC CTTTTTGAAGCACGTACATTTTGTAACAAAGAACTGAA GCTCTTATTATATTATTAGTTTTGATTTAATGTTTTCAG CCCATCTCCTTTCATAT
4	CYP3A4_SNP12	5' region [-747C>G]	Possible association (OR 12.067, 95% CI 1.491-97.692, p=0.020) with increased risk of prostate cancer	AAGTCACCAGAAAGTCAGAAGGGATGACATGCAGAG GCCCAGCAATCTCAGCTAAGTCAACTCCACCAGCCTT TCTAGTTGCCCACTGTGTGTACAGCAC(C/G)CTGGTA GGGACCAGAGCCATGACAGGGAATAAGACTAGACTA TGCCCTTGAGGAGCTCACCTCTGTTCAGGGAAACAG GCGTGGAAACACAATGGTGGTA
5	CYP3A4_SNP13	Intron 7 [IVS7 -202C>T]		CTGTAGTCCAATAGATAAAGGCAAAGAGATTAGGGCA TTGAATTTTGTTCCTTTTATCCTTCAAAGATGCACAA GGGGCTGCTGATCTCACTGCTGTAG(C/T)GGTGCTCC TTATGCATAGACCTGCCCTTGCTCAGCCACTGGCCTG AAAGAGGGGCAAAGTCATAGAAGGAATGGCTTCCA

				GTTGAGAACCTTGATGTCT
6	CYP3A4_SNP15	2204 base pairs after the stop codon, G>C	Possible association (OR 0.41, 95% CI 0.22-0.79, p=0.007) with prostate cancer	GAACTATTGGAACTGATAAACACATTCAGTAAAGTTG CAGGATACAAAATCAGCATACAAAAATCAGTAGCATT TCTATATGCCAATAGTGAACAATCTG(G/C)CAAAAATA AAAAAGTAATCCCATTTACAATAGCCACAAATAAAACT AAATACCTAGAAATTAACTTAATCAAAGAAGAGAAAG GTCTCTACAATGAATAC
7	CYP3A4_SNP19	Intron 2 [IVS2 -132C>T]		ATAAGTCATTCAGTATCCACAACACTTGGAGAGAATT CAAGAGTGATTTTAAATTTCCCTTTTCAAATACCTCCT CTGTTTTCTCTTATTTCCTTTATGA(C/T)GTCTCCAAAT AAGCTTCCTCTAACTGCCAGCAAGTCTGATTTCATTG GCTTCGACTGTTTTCATCCCAATTAGAGGCAGGGTTA AGTACATTAAAAATAA
8	CYP3A4_SNP21	Intron 1 [IVS1 -868C>T]		AACTGCCCCTAGGATCCAATCATCTCCTACCAGGCCC CACCTCCAGTATTGGGGATTGCATTTCAACATGAGAT TTTGGTAGGGGCACAGATTCAGACCATAT(C/T)ACTG GCACTGTGCTAATCAGATGAATATCACCAGTTGGAAG GCTAGATTCCACAAGAGGAGGAATGACCTGGAAATT GGTTCTTTAGTTGTGATTCT
9	CYP3A4_SNP22	5' region [-847A>T]		GGGGTCCCCTTGCCAACAGAATCACAGAGGACCAGC CTGAAAGTGCAGAGACAGCAGCTGAGGCACAGCCAA GAGCTCTGGCTGTATTAATGACCTAAG(A/T)AGTCACC AGAAAGTCAGAAGGGATGACATGCAGAGGCCCAGCA ATCTCAGCTAAGTCAACTCCACCAGCCTTTCTAGTTG CCCACTGTGTGTACAGCACCC
10	CYP3A4_SNP24	766 base pairs after the stop codon, delT		TCAGGCACAGTGGCTCACGCCTGTAATCCTAGCAGTT TGGGAGGCTGAGCCGGGTGGATCGCCTGAGGTCAG GAGTTCAAGACAAGCCTGGCCTACATGG(T/-) TGAAACCCCATCTCTACTAAAAATACACAAATTAGCTA GGCATGGTGGACTCGCCTGTAATCTCACTACACAGG AGGCTGAGGCAGGAGAATCACTTGAA
11	CYP3A4_SNP25	1454 base pairs after the stop codon, C>T	Possible association (OR 6.54, 95% CI o.99-43.10, p=0.05) with prostate cancer	TGGGTGTGGGAGTCCAAGCAAGCAGAGAAGGGGTC GACGCAGAGGGGTGGCTTGCAAGAGCAGCCAGAGC CTAAATAGGGTATGGAGAACCCACATGAGG(C/T)GAG GAGGGCATCCATGAGTGGGAGGGGTTGGGTGAGGT TTGGCTACATAAAGGGGATTGATCAAATAAGTAAATG TATTAAGGATGATAGAAGCCAGGCT
12	CYP3A4_SNP26	Intron 3 [IVS3 +1992T>C]		TTGCATTTCTCTAATGACCAGTGATGATGAGCATTTTT TCACATGTCTGTTGGCTGCATAGATGTCTTCTTTTGA GAAGTGTCTGTTCATATCCTTTGCC(T/C)ATTTTTTGAT

				GGGGTTGTTTGCTTTTTTTTCTTGTAAATTTGTTTAAGT TCTTTGTAGATTCTGGATGTTAGCCCTTCGTCAGATG GATAGATTGCAAAAA
13	CYP3A4_SNP27	Intron 9 [IVS9 +841T>G]		TAACTATTGGTTCTAGAGAGCAGGACTGGGCTTACTC CAGCATACTGCTTTAAATATATCCATGTCTACATCCAC TTTTGTCTGTATGTCTATGTATCTA(T/G)CTATGTATCT ATCTAGCTATGTATCTATCTATCTATCTATCTATCATCT ATCTATCTATCTATCATCTATCCATCTATCATCAT TTATCCATCTAT
14	CYP3A4_SNP28	Intron 12 [IVS12 -473T>G]		CTTCCCATCTTTACACTGGATGGGTTCAATTGGGAGG AATTACTGGACTCTGGAAGTTGAAGACTGTCCATATA ATTAAAATGTACAATAACTACCCAGG(T/G)TTACCTTG CAAGTTTCAACATACACACAAAATTAACTTTATATGACTC TTCAAAAACAGTTTGCCATCATACCTAATAATCTGGTT TAAATTTTAAAAACTC
15	CYP3A4_SNP29	Intron 12 [IVS12 +581C>T]		TGCCCAGAGTGTGGCTTTAAAAGCTTCCCCATTGCTT CTCATGTGAAGCCAAGGTTGAGAATGACTAATTTAAG GCATTTCTGGTGGATATAAAGGACTA(C/T)CACAGTCC AAGGCCATCCTGACTGACCTCACCTTCCAGGTGCCTA GCTCCATCCAGCTGGGCTCCTTTTCAACCCAATTATA ACTCTATTAATGTTGTTC
16	CYP3A4_SNP30	Intron 12 [IVS12 +586G>A]		AGAGTGTGGCTTTAAAAGCTTCCCCATTGCTTCTCAT GTGAAGCCAAGGTTGAGAATGACTAATTTAAGGCATT TCTGGTGGATATAAAGGACTACCACA(G/A)TCCAAGG CCATCCTGACTGACCTCACCTTCCAGGTGCCTAGCTC CATCCAGCTGGGCTCCTTTTCAACCCAATTATAACTC TATTAATGTTGTTCCCAGC
17	CYP3A4_SNP31	Intron 12 [IVS12 +646C>A]		TAATTTAAGGCATTTCTGGTGGATATAAAGGACTACC ACAGTCCAAGGCCATCCTGACTGACCTCACCTTCCAG GTGCCTAGCTCCATCCAGCTGGGCTC(C/A)TTTTCAA CCCAATTATAACTCTATTAATGTTGTTCCCAGCCAGG CATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGA GGCCGAAGCAGGCGGATCA
18	CYP3A4_SNP32	Intron 3 [IVS3 -734G>A]		CTAATTTGATTGCACTGTGGTCTGAGAGACAGTTTGT TATGATTTCTGTTCTTTTACATTTGCTGAGGAGTGCTT TACTTCCAATTATGTGGTCAATTTT(G/A)GAATAAGTG CGATGTGGTGCTGAGAAGAATGTATATTCTGTTGATT TGGGGTGGAGAGTTCTGTAGATGTCTATTAGGTCCG CTTGGTGCAGAGCTGAGT

19	CYP17_SNP1	Intron 1 [IVS1 -271A>C]		GGACAGGCATAGTTTAGAGAGTTTATCCCATCCAGAG TTGCCTTCTGTGGTCAGAAACTGATGAGCAAAAAGAA GCCCAGAGGGCACCCTGTCAGCGAA(A/C)AGAACCC CAATGCTGCTGCATTCTAATTAAGGGTTCTTTCTTTCT CCTTGATCTACTGTATTTCTGAAGGAATTGGGAGTAG GAGGCCTTAGGGTCTGTC
20	CYP17_SNP3	Intron 5 [IVS5 +75C>G]		TGGCCTTCCTGCTGCACAATCCTCAGGTGTGCTTCCC CCTCATTGATCCTAGACCCCAGCCAGCCCAATCTCTG GGCTCCAGAGAAAGGGAGAGCCAATT(C/G)TCTCAGG CTTTCTGTGCAGGAAGACTAGGCCTGCCCTGCTCCTT ACCCAAGCAGTAGTTGGCTTTGACCCCAGAGTAGAG CTGCCCCATCTTCTGGAAGC
21	CYP17_SNP4	Intron 1 [IVS1 +426G>A]		CAGCACTTAGCCTAGCACCCAGCACAGTAAGTGCCC CTTATACAGCCAGGATTCATGTTACTTTTCATGGAAAA TGGGGGCAGTGACTACTGTCCTCCAT(G/A)AAAGCTG CTGGGGAGAATTAGCCTAGCTATTGCAGGCTGGGAT TGCTGCTTTCCTGGTGCTATTTCCAGCTACTCAGGCT CACAGGGGCAGTTTTCTACA
22	CYP17_SNP6	Intron 1 [IVS1 -99C>T]	Possible association (OR 2.130, 95% CI 1.141-3.977, p=0.018) with increased risk of prostate cancer	ATTGGGAGTAGGAGGCCTTAGGGTCTGTCCTACCAA GTCCTTGCAGTCATGGTGGAGTGCAGTGGGGCTGTG CCCACATGGGAGTCAGCATGCCAGGTAC(C/T)TGCCT TCTCCTCCAGGAAGGAAAGCAGGGACCAGAGGTGTA AGGGCAAGAGTGGGGTGGATGGTGTGAGATTCCTAC AGCCTTGCCTGCTCTCTAAAGGC
23	CYP17_SNP8	Intron 1 [IVS1 -700C>G]		GCCACTGTGCCCTGCCAGCCTCTCAGCTTTGATCAA GCCAAGGGTTGGTTTATTTTTTCTTGGACCAATCAGC CAGGTCTGCTGACCAACTACCTAGCTC(C/G)CACCTC TGCTGGCTTCCTCCCGGGGGCAGAGAAGATGGAGAA GGCTAGTCATGTGGATCTTCAGGGTCAGGAAATGGA AAAGGGAGGCTTTGGACCCTTT
24	CYP17_SNP11	Intron 1 [IVS1 -565G>A]		ATGGAGAAGGCTAGTCATGTGGATCTTCAGGGTCAG GAAATGGAAAAGGGAGGCTTTGGACCCTTTTGCTTTG GGGGGCACCTCTAGGAGGAGGCAGCTC(G/A)GCCCA AGTCCAGACTGGGTAGACAAAACATCTGCACTCTCCA AATGTGGGCTTGTGGCTGGGTATGCAGGCTTGCAAT GGAAGGGTAAACCTGAGTGAGG
25	CYP17_SNP12	Intron 3 [IVS3 +141A>T]		CTGACATTGTCCCCAATCTTCCTTCCTTTTTACTTCCC TGCTCCAGCCGCAATGACCCATCTTTTTCCTGATTAC CTCCGCCACCTCTACCTCCTCTGCC(A/T)CTTAAAACC TTTGCCATTTCTCTGCAGAGATAGATTTAGCCTTTTAA

				TTATGCACCTTAGTACTCCAGATAATGACCTTCATTTC TTTTCCAATTACCAT
26	CYP17_SNP18	5' region [-1488C>G]		ATTTTTAGGGAACAAGGGAAAACAACCATAAGGTCTG ACTGCCTGCAGGGTCGGGCAGAAAGAGCCATATTTT CCTTCTTGAGAGAGGCTATAAATGGA(C/G)ATGCAAG TAGGGAAGATATCACTAAATTCTTTTCCTAGCAAGGA GTATTATTATTAATACCCTGGGAAAGGAATGCATTCCT GGGGGGAGGTCTATAAACA
27	CYP17_SNP19	5' region [-1204C>T]		TAGGGTGGGGAAAAACTCCGCCCTGGTAAATTTGTG GTCAGACCGGTTCTCTGCTGTCGAACCCTGTTTGCTG TTGTTTAAGGTGTTTATCAAGACAGTA(C/T)GTGCACC GCTGAACATAGACCCTCATCTGTAGTTCTGCTTTTGC CCTTTGCCTTGTGATCTTTGTTGGACCCTTATCAGTG GTTCTGCTTTTGCCCTTTG
28	CYP17_SNP20	Intron 1 [IVS1 +466G>A]		TACAGCCAGGATTCATGTTACTTTTCATGGAAAATGG GGGCAGTGACTACTGTCCTCCATAAAAGCTGCTGGG GAGAATTAGCCTAGCTATTGCAGGCTG(G/A)GATTGC TGCTTTCCTGGTGCTATTTCCAGCTACTCAGGCTCAC AGGGGCAGTTTTCTACAATGACATTTCAGGGTTGCTG ATGAGCCTCCCACTCAGCAG
29	CYP17_SNP42	712 base pairs after the stop codon, G>A		CTGGAGGATTTTAAGTATGTAAGTGGAACAATCTGTT TTTTTGTTTTTGTTTTTGTTTGAGAAGGAGTTTCGCTC TTGTTGCCCTGGCTGGAGTGCAATG(G/A)CATGATCT TGGCTCACTGCAACCCCTGCCTCCTGAGTTCAAGTGA TTCTCCTGCCTCAGCCTCCAAAATAGCTGGGATTGCA GGCGTGTGCCACCATGCC
30	SRD5A2_SNP2	1356 base pairs after the stop codon (3' UTR), A>C		TCTTGTGAAGGGGTCACCCCAGCATGAGTGCTGAGA TATGGACTCTCTA(A/C)GGAAGGGGCCGAACGCTTGT AATTGGAATACATGGAAATATTTGTCTTCTCAGGCCTA TGTTTGCGGAATGCATTGTCAATATTTAGCAAACTGTT TTGA
31	SRD5A2_SNP4	849 base pairs after the stop codon (3' UTR), A>G		CGAGAACAGTTTTACAATAGACATTGCAAACTCTCAT GTTTTTGGAAACT(A/G)GTGGCAATATCCAAATAATGA GTAGTGTAAAACAAAGAGAATTAATGATGAGGTTACA TGCTGCTTGCCTCCACCAGATGTCCACAACAATATGA AGTAC
32	SRD5A2_SNP30	5' region [-870G>A]		GTCTGCGTGTATGACGGCTAGACAGGAGTTCAGAGA ACAGCGGGGTCGCCAGGCCACCACCTGATGGGCCA CGGCTCATTGGCTCTAGGAGCTGGGAAAG(G/A)GCAT CCCAGGAAAGAAGCCCTAGACTTTAGCCTGAGTCTG

				GGCCACTCTAGGGGACCGGGAGTGGGGTGGCGGGA GAGGACGCGCAGAATCTCGACTTCT
33	SRD5A2_SNP31	5' region [-2036(A)7-8]		AGCTAATTGTTATAATAGTGGAGAAAAGATCATGAGG ACAAAAAGTGGGCAGAGTCGGAAGAAAAGAGAGGAA GAAATTGAGACAGAAGACATTTCATTT[A_7/A_8]TATTCCA TTGAGCTGGGTTTGAAATAGTGCACTGCCTGTTCTCC TAATGCTGTATGGTGTCATGAAATCTATTGTTTACTGA GTCTATGAGCC
34	SRD5A2_SNP32	545 base pairs after the stop codon (3' UTR), T>C		AACTCTGAAGCCACAAAGACCCAGAGCAAACCCACT CCCAAATGAAAACCCCAGTCATGGCTTCCTTTTTCTT GGTTAATTAGGAAAGATGAGAAATTAT(T/C)AGGTAGA CCTTGAATACAGGAGCCCTCTCCTCATAGTGCTGAAA AGATACTGATGCATTGACCTCATTTCAAATTTGTGCAG TGTCTTAGTTGATGAGTG

Table 2(b) : Public SNPs

SNP Present in Seq ID Number	Public SNPs	Location	Comment	
35	SRD5A2_SNP12 (NCBI ss#543530; rs#413836)	Intron 2 [IVS2 +626C>T]	Possible association (OR 3.006, 95% CI 1.231-7.343, p=0.016) with increased risk for progression of prostate cancer	AAAGAAACATTGTTTCTTAAAACAATGTTTTAAGAAAG TGTACGAATTTGTGTCAGGCCACATCCAAAACTGTCC TGGGCTGCATGTGGCCCACAGGCTG(C/T)GGGTTGG ACAAGCCTGGCCTAGAAGGCTTTGCCCCCATGTATTC ATGGGGGTTGGTTCCTCACTTTATTTAGTTCCCTACC AATTTGCACCTCCTCAAAGGGACTTTCCC
36	SRD5A2_SNP17 (NCBI ss#1037918; rs#545303)	5' region [-8029C>T]	Possible association (OR 0.308, 95% CI 0.126-0.750, p=0.010) with increased risk for progression of prostate cancer	GGGAACTCACAGTTTTTTGGCTGTCTCATAGAGTTTG CAACAGTAAAACTGCTTCTTTCAAAGGGTCTGTGAAT TCTTTCAGTTTTCCTGGTATGTTCCCATGGTAGTTCTT GCAGCAAAAG(C/T)TCACAGTGTGAGTCTCCACACAC TGTTCTGTCCATTCCAAGCAGGAGCTGCATGTTAGTT CTGTCTGCTATCCACCATTTTCCAATTTTG
42	CYP3A4_SNP1 (NCBI	Intron 7 [IVS7 +34T>G]	Possible association (OR 0.21, 95% CI	CCCTTTGTGGAAAACACCAAGAAGCTTTTAAGATTTG ATTTTTTGGATCCATTCTTTCTCTCAATAAGTATGTGG

	ss#6903779 ; rs#2687116)		0.05-0.86, p=0.03) with prostate cancer	ACTACTATTTCCTTTTATTTATCTT(T/G)CTCTCTTAAAA ATAACTGCTTTATTGAGATATAAATCACCATGTAATTC ATCCACTTAAAATATACAGTTCAGTGATTTGTAGTACA TTTGAAGATATGT
43	CYP3A4_SNP47 (NCBI ss#2723639 ; rs#1851426)	5' region [-1232C>T]	Possible association (OR 0.19, 95% CI 0.06-0.62, p=0.006) with prostate cancer	TTGGGTGTGTGGCGGGTGTGTCCGCGTTTTAAAAAG CGCCGCACGCTTTGAACTCCAATTCCACCCCCAAGA GGCTGGGACCATCTTA(C/T)TGGAGTCCTTGATGCTG TGTGACCTGCAGTGACCACTGCCCCATCATTGCTGG CTGAGGTGGTTGGGGTCCATCTGGCTATCTGGGCAG CTGTTCTCTTC
44	SRD5A2_SNP26 (NCBI ss#1037925 ; rs#676033)	5' region [-3001G>A]	Possible association (OR 1.57, 95% CI 1.08-2.30, p=0.02) with prostate cancer	ACTATTCTCCTGCCCTAATCAGCCAGGTCCAGGTAAC AGAAAAGTAAAGACAGCCGCTGTACCCCAGAGCCTG CTAAAAGTATTCAAACGAGCTAATCCTAAGCCTGATTA CCTTGTCATGCCCACTCTTTCCTGCAGAAACTACAGT AA AGGCTCTTGCCCACCTTGACCCCTCACTCC (G/A) GCTGCCTCCTAACACTGGTGCTTCTCCATGTGGTCTT GGGTGGTGTGCTGTGTCTTCTGTTTGTAGGGATCTGT CGATATAAACCTTTTC CTTCACGATA
45	SRD5A2_SNP1 (NCBI ss# 4403959; rs# 1042578)	1552 bp after the stop codon, G>A	Possible association (OR 0.52, 05% CI 0.27-1.00, p=0.05) in the European American population	GGTACTAAGCACAGAAACTCACTATATAAGTCACATA GGAAACTTGAAAGGTCTGAGGATGATGTAGATTACTG AAAAAT(G/A)CAAATTGCAATCATATAAATAAGTGTTTT TGTTGTTCATTAAATACCTTTAAATCATGGATGTAAGC AGTTTGTTGATA

[#] SNP was discovered in the Coriell Diversity Set and was not present in the 276 individuals from prostate cancer sibships (still obviously a real SNP since it's seen in the Diversity Set)

[@] ambiguous genotyping results; SNP was excluded from all further analyses. However, most likely real SNPs

The numbering system for the location of SNPs is according to the common mutation nomenclature (den Dunnen and Antonarakis (2000) Human Mut 15, 7-12; http://www.dmd.nl/mutnomen.html#DNA).

Table 3. The origins, nucleotide changes and allele frequencies of single nucleotide polymorphisms (SNPs) in *CYP17*, *CYP3A4*, and *SRD5A2* observed in the Coriell Diversity set (CDS), European Americans, and African-Americans.

SNP	Origin [a]	Nucleotide Change [b]	c	d	Allele Frequency				
					CDS	European Americans		African-Americans	
						Ctrls	Cases	Ctrls	Cases
CYP17									
SNP18	Novel (C+C)	-1488C>G	B	I	.26	NA [e]	NA	NA	NA
SNP19	Novel (C+C)	-1204C>T	B	I	.10	NA	NA	NA	NA
SNP29	dbSNP / HGVbase (-)	-34T>C	1,2,3	II	.44	.40	.38	.33	.38
SNP30	GeneSNPs / dbSNP (-)	C22W (66C>G)	B	I	-	NA	NA	NA	NA
SNP31	GeneSNPs / dbSNP / HGVbase (-)	H46H (138C>T)		I	.43	.43	.36	.41	.35
SNP32	GeneSNPs / dbSNP / HGVbase (-)	S65S (195G>T)		I	.46	.44	.33	.40	.32
SNP4	Novel (C+C)	IVS1 +426G>A	1	II	.27	.40	.39	.30	.36
SNP20	Novel (C+C)	IVS1 +466G>A	4	II	.06	.03	.01	.02	.02
SNP8	Novel (C+C)	IVS1 -700C>G		I	.19	.14	.15	.21	.08
SNP26	GeneSNPs / dbSNP (+<)	IVS1 -679C>T	D	I	-	.06	.02	.04	.01
SNP11	Novel (CDS)	IVS1 -565G>A	A	I	.04	-	-	-	-
SNP1	Novel (C+C)	IVS1 -271A>C		I	.44	.46	.40	.40	.43
SNP6	Novel (C+C)	IVS1 -99C>T	2	II	.38	.29	.28	.11	.15
SNP23	HGMD (*)	S106P (316T>C)	A	I	-	-	-	-	-
SNP25	HGMD (*)	IVS2 +5G>T	A	I	-	-	-	-	-
SNP7	dbSNP (R)	IVS2 +105A>C	1	II	.46	.29	.28	.13	.15
SNP22	dbSNP (+ <)	IVS2 -83C>T	1	II	.04	.002	.0008	.06	.09
SNP24	HGMD (+ <)	E194X (580G>T)	D	I	-	-	-	-	.01
SNP5	dbSNP (R)	IVS3 +35T>C		I	.06	.16	.16	.20	.07
SNP12	Novel (C+C)	IVS3 +141A>T		I	.04	.04	.02	-	.01
SNP21	GeneSNPs /dbSNP (*)	D283D (849C>T)	A	I	-	-	-	-	-
SNP3	Novel (C+C)	IVS5 +75C>G	1	II	.33	.40	.39	.20	.23
SNP33	HGMD (-)	IVS7 +5G>A	D	I	-	-	.02	-	-
SNP34	HGMD (*)	F417C (1250T>G)	A	I	-	-	-	-	-

SNP35	GeneSNPs / dbSNP / HGVbase (-)	P428P (1284G>A)	B	I	-	NA	NA	NA	NA
SNP36	HGMD (*)	R440H (1319G>A)	A	I	-	-	-	-	-
SNP37	HGMD (*)	R496C (1486C>T)	A	I	-	-	-	-	-
SNP42	Novel (CAP)	stop + 712G>A		I	-	.28	.18	.18	.21
SNP16	GeneSNPs (R)	stop +2074G>A	D	I	.06	.01	.02	-	.03
CYP3A4									
SNP48	GeneSNPs (*)	-8086G>A	A	I	-	-	-	-	-
SNP49	GeneSNPs (-)	-6790G>A	B	I	.50	NA	NA	NA	NA
SNP47	dbSNP (R)	-1232C>T	1	II	.19	.05	.04	.56	.56
SNP22	Novel (CDS)	-847A>T		I	.06	-	-	.20	.15
SNP12	Novel (CAP)	-747C>G	1,2	II	-	.08	.08	.01	.04
SNP11	HCANC (+)	-392A>G	3	II	.13	.04	.04	.58	.54
SNP45	HGVbase (*)	-290A>G	A	I	-	-	-	-	-
SNP50	GeneSNPs (*)	-26G>A	A	I	-	-	-	-	-
SNP21	Novel (CDS)	IVS1 -868C>T		I	NA	-	.009	.18	.17
SNP20	dbSNP (R)	IVS2 +671T>A		I	.15	.07	.07	.42	.44
SNP19	Novel (CDS)	IVS2 -132C>T	D	I	.02	-	.009	-	-
SNP26	Novel (C+C)	IVS3 +1992T>C	B	I	.40	NA	NA	NA	NA
SNP32	Novel (CDS)	IVS3 -734G>A	B	I	NA	NA	NA	NA	NA
SNP33	GeneSNPs (+ <)	IVS4 –172G>A	A	I	.02	-	-	-	-
SNP17	HCANC (*)	S222P (664T>C)	A	I	-	-	-	-	-
SNP1	dbSNP (R)	IVS7 +34T>G	1	II	.17	.06	.05	.62	.56
SNP14	dbSNP (R)	IVS7 +526C>T		I	.02	-	.02	.11	.11
SNP13	Novel (C+C)	IVS7 -202C>T	1	II	.31	.14	.13	.66	.72
SNP2	Novel (C+C)	IVS9 +187C>G	B	I	.08	NA	NA	NA	NA
SNP27	Novel (C+C)	IVS9 +841T>G		I	.06	-	.01	.07	.08
SNP46	HGVbase (+ <)	M318I (954G>A)	B	I	-	NA	NA	NA	NA
SNP10	dbSNP (R)	IVS10 +12G>A		I	.42	.16	.14	.67	.66
SNP34	GeneSNPs /dbSNP (*)	I431T (1292T>C)	A	I	-	-	-	-	-
SNP18	HCANC (*)	M445T (1334T>C)	A	I	-	-	-	-	-
SNP29	Novel (CDS)	IVS12 +581C>T	A	I	.02	-	-	-	-
SNP30	Novel (CDS)	IVS12 +586G>A	D	I	.02	.04	.01	-	.01

SNP31	Novel (CDS)	IVS12 +646C>A	A	I	.02	-	-	-	-
SNP28	Novel (C+C)	IVS12 -473T>G		I	.08	.006	.01	.24	.27
SNP24	Novel (C+C)	stop + 766delT; T>G	1	I	.33	.14	.13	.52	.53
SNP6	Novel (CAP)	stop +945A>T	D	I	-	.02	.02	-	-
SNP25	Novel (CDS)	stop + 1454C>T	1	II	.08	.003	.006	.23	.28
SNP5	Novel (C+C)	stop + 1639A>T	1	II	.63	.17	.16	.61	.62
SNP15	Novel (C+C)	stop + 2204G>C	1	II	.13	.13	.11	.24	.20
SRD5A2									
SNP17	GeneSNPs (R)	-8029C>T	1,2	II	.33	.46	.46	.46	.37
SNP18	GeneSNPs (*)	-7819G>C	A	I	-	-	-	-	-
SNP26	GeneSNPs (+)	-3001G>A	1	II	.30	.29	.30	.27	.39
SNP28	GeneSNPs (*)	-2851A>T	A	I	-	-	-	-	-
SNP31	Novel (C+C)	-2036(A)7-8, A>T	C	I	NA	.29	.28	.43	.33
SNP5	GeneSNPs (R)	-1971G>A	B	I	.48	NA	NA	NA	NA
SNP30	Novel (CAP)	-870G>A	D	I	-	.01	.02	-	.01
SNP21	HGMD (*)	G34R (100G>A)	A	I	-	-	-	-	-
SNP22	GeneSNPs / dbSNP / HGVbase (-)	A49T (145G>A)	1,3	II	NA	.04	.04	.01	.03
SNP20	GeneSNPs / dbSNP / HGVbase (-)	V89L (265G>C)	1,3	II	NA	.29	.29	.32	.34
SNP23	GeneSNPs / dbSNP (-)	IVS1 +15C>T	B	I	.46	NA	NA	NA	NA
SNP11	GeneSNPs / dbSNP (-)	IVS1 +24664G>T		I	.48	.24	.27	.19	.22
SNP12	GeneSNPs / dbSNP (-)	IVS2 +626C>T	1,2	II	.48	.41	.40	.27	.30
SNP7	HGMD (*)	G183S (547G>A)	A	I	-	-	-	-	-
SNP8	HGMD (*)	N193S (578A>G)	A	I	-	-	-	-	-
SNP9	HGMD (*)	P212R (635C>G)	A	I	-	-	-	-	-
SNP10	HGMD (*)	IVS4 +1G>T	A	I	-	-	-	-	-
SNP32	Novel (CAP)	stop +545T>C	D	I	-	-	.005	-	-
SNP4	Novel (C+C)	stop +849A>G		I	.13	.11	.12	.16	.23
SNP2	Novel (C+C)	stop +1356A>C	D	I	.02	.006	.009	-	-
SNP1	GeneSNPs (R)	stop +1552G>A	1	II	.16	.12	.12	.19	.23
SNP13	GeneSNPs (+)	stop +3059G>A	1	II	.13	.09	.09	.13	.14
SNP14	GeneSNPs (-)	stop +5179A>C	D	I	.02	.01	.005	-	-

SNP15	GeneSNPs (-)	stop +9301G>C	1	II	.46	.26	.27	.21	.23
SNP16	GeneSNPs (-)	stop +9502C>T	D	I	-	.006	-	-	-

[a] Explanations: (*), SNP did not show up in our study population; (R), rediscovered; (+), we had sequence coverage but did not rediscover the SNP; (+ <), we had sequence coverage but did not rediscover the SNP, most likely due to the low minor allele frequency; (-), we did not have sequence coverage explaining why we did not rediscover the SNP; (CDS), novel SNP discovered originally in the Coriell Diversity Set; (CAP), novel SNP discovered originally in the prostate cancer sibships; (C+C), novel SNP discovered originally in both populations

[b] Underlined bases indicate the allele for which frequencies are given

[c] Excluded from haplotyping in Phase I and from consideration for Phase II based on (A) being monoallelic in the prostate cancer sibships, (B) yielding ambiguous genotyping results, (C) low success rate, (D) allele frequency <5%. Included in Phase II association analyses based on (1) being a haplotype tagging SNP, (2) case-control difference in Phase I, (3) previous publications supporting association, (4) SNP conveniently located within the same PCR fragment as another included SNP

[d] I, allele frequencies based on 276 samples; II, allele frequencies based on 1117 samples

[e] NA, data not available

Table 4A. All non-stratified association results between *CYP17, CYP3A4,* and *SRD5A2* variants and risk of prostate cancer among cases and sibling controls [a]

Genes	Genotype Comparison [b]	All Subjects (n=886...920)		European Americans (n=781...834)		African-Americans (n=74...76)	
		OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value
CYP17							
SNP29	CC or TC vs. TT	0.91 (0.65-1.29)	0.61	0.86 (0.59-1.25)	0.42	1.96 (0.72-5.31)	0.19
SNP4	AA or GA vs. GG	0.88 (0.62-1.25)	0.47	0.82 (0.56-1.19)	0.30	1.96 (0.72-5.31)	0.19
SNP20	AA or GA vs. GG	0.57 (0.25-1.31)	0.19	0.52 (0.21-1.28)	0.15	1.87 (0.55-6.35)	0.31
SNP6	TT or CT vs. CC	0.90 (0.64-1.27)	0.56	0.81 (0.57-1.17)	0.27	2.38 (0.71-7.92)	0.16
SNP7	CC or AC vs. AA	0.84 (0.59-1.19)	0.33	0.77 (0.53-1.11)	0.16	2.00 (0.59-6.72)	0.27
SNP22	TT or CT vs. CC	1.99 (0.67-5.86)	0.21	NA [c]	NA	1.69 (0.43-6.68)	0.45
SNP3	GG or CG vs. CC	0.90 (0.63-1.27)	0.54	0.81 (0.56-1.19)	0.28	2.23 (0.76-6.54)	0.14
CYP3A4							
SNP47	TT or CT vs. CC	0.59 (0.31-1.09)	0.09	0.60 (0.29-1.23)	0.16	0.56 (0.17-1.86)	0.34
SNP12	GG or CG vs. CC	1.51 (0.92-2.50)	0.11	1.44 (0.86-2.38)	0.16	NA	NA
SNP11	GG or AG vs. AA	0.76 (0.43-1.36)	0.36	0.83 (0.41-1.66)	0.59	0.61 (0.23-1.63)	0.32
SNP1	GG or TG vs. TT	0.53 (0.29-0.99)	**0.05**	0.57 (0.28-1.18)	0.13	0.44 (0.13-1.57)	0.21
SNP13	TT or CT vs. CC	0.79 (0.51-1.22)	0.29	0.71 (0.45-1.12)	0.14	2.33 (0.42-12.84)	0.33
SNP24	GG or TG vs. TT	0.95 (0.62-1.44)	0.79	0.88 (0.56-1.36)	0.56	1.81 (0.45-7.25)	0.40
SNP25	TT or CT vs. CC	1.59 (0.58-4.39)	0.37	NA	NA	1.21 (0.37-3.98)	0.75
SNP5	TT or AT vs. AA	0.86 (0.56-1.31)	0.47	0.74 (0.48-1.15)	0.19	4.48 (0.67-30.07)	0.12
SNP15	CC or GC vs. GG	0.69 (0.46-1.05)	0.09	0.68 (0.44-1.05)	0.08	0.82 (0.22-3.03)	0.77
SRD5A2							
SNP17	TT or CT vs. CC	0.87 (0.58-1.29)	0.48	0.93 (0.61-1.41)	0.74	0.21 (0.04-1.12)	0.07
SNP26	AA or GA vs. GG	1.57 (1.08-2.30)	**0.02**	1.59 (1.08-2.34)	**0.02**	1.00 (0.19-5.31)	1.00
SNP22	AA or GA vs. GG	0.84 (0.38-1.85)	0.66	0.90 (0.40-2.02)	0.79	NA	NA
SNP20	CC or GC vs. GG	1.56 (1.08-2.25)	**0.02**	1.47 (1.00-2.16)	**0.05**	2.29 (0.81-6.50)	0.12

SNP12	TT or CT vs. CC	1.00 (0.69-1.46)	0.98	0.98 (0.67-1.44)	0.94	0.94 (0.18-4.97)	0.94
SNP1	AA or GA vs. GG	0.81 (0.53-1.24)	0.33	0.83 (0.53-1.31)	0.43	1.20 (0.23-6.21)	0.83
SNP13	AA or GA vs. GG	0.94 (0.61-1.47)	0.80	0.98 (0.61-1.55)	0.92	1.64 (0.25-10.54)	0.61
SNP15	CC or GC vs. GG	1.14 (0.79-1.63)	0.49	1.14 (0.79-1.65)	0.49	0.77 (0.15-3.94)	0.75

[a] From conditional logistic regression, with matching on family, and a variance estimator that incorporates sibling correlations.
[b] All results are from dominant models that compare homozygous and heterozygous carriers of variant versus the homozygous wildtype (OR=1.0).
[c] NA, data not available

Table 4B. Statistically significant allele associations obtained from analysis stratified by aggressiveness [a]

SNP	Stratification	All Subjects (n=443...465)		European Americans (n=394...418)		African-Americans (n=39)	
		OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value
CYP3A4							
SNP47	Low TNM and grade	0.19 (0.06-0.62)	**0.006**	0.07 (0.01-0.53)	0.10	0.66 (0.14-3.04)	0.59
SNP11	Low TNM and grade	0.20 (0.06-0.67)	**0.009**	0.08 (0.01-0.59)	0.13	0.66 (0.14-3.04)	0.59
SNP1	Low TNM and grade	0.21 (0.05-0.86)	**0.03**	0.16 (0.03-0.82)	**0.03**	0.65 (0.03-16.26)	0.80
SNP25	Low TNM and grade	6.54 (0.99-43.10)	**0.05**	NA [b]	NA	6.57 (1.26-34.17)	**0.03**
SNP5	Low TNM and grade	0.57 (0.30-1.10)	0.09	0.51 (0.26-0.99)	**0.05**	NA	NA
SNP15	Low TNM and grade	0.41 (0.22-0.79)	**0.007**	0.52 (0.27-1.01)	0.06	NA	NA
SRD5A2							
SNP1	Low TNM and grade	0.59 (0.32-1.10)	0.09	0.52 (0.27-1.00)	**0.05**	1.41 (0.18-10.79)	0.74

[a] From conditional logistic regression, with matching on family, and a variance estimator that incorporates sibling correlation.
[b] NA, data not available

Table 5A. All non-stratified haplotype association results for *CYP17*, *CYP3A4*, and *SRD5A2* [a].

Haplotype	All Subjects (n=920)		European Americans (n=834)		African-Americans (n=76)	
	OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value
CYP17						
Hap1	1.0	-	1.0	-	1.0	-
Hap2	0.83 (0.61-1.12)	0.22	0.80 (0.58-1.10)	0.17	2.63 (0.45-15.33)	0.28
Hap3	1.07 (0.67-1.70)	0.78	1.09 (0.65-1.83)	0.74	1.41 (0.49-4.08)	0.52
Hap4	0.85 (0.56-1.31)	0.47	0.84 (0.51-1.40)	0.51	1.02 (0.43-2.42)	0.97
CYP3A4						
Hap1	1.0	-	1.0	-	1.0	1
Hap2	1.25 (0.74-2.08)	0.41	1.16 (0.69-1.96)	0.57	NA [b]	NA
Hap3	1.20 (0.70-2.03)	0.51	1.07 (0.62-1.82)	0.82	3.34 (0.49-22.89)	0.22
Hap4	0.46 (0.21-1.01)	**0.05**	0.44 (0.20-0.96)	**0.04**	0.99 (0.06-16.37)	0.99
Hap5	1.08 (0.78-1.50)	0.66	1.05 (0.74-1.51)	0.77	1.86 (0.60-5.75)	0.28
SRD5A2						
Hap1	1.0	-	1.0	-	1.0	-
Hap2	1.14 (0.82-1.60)	0.43	1.12 (0.80-1.58)	0.50	2.57 (0.43-15.52)	0.30
Hap3	0.76 (0.48-1.21)	0.25	0.81 (0.51-1.30)	0.39	NA	NA
Hap4	1.13 (0.72-1.77)	0.61	1.03 (0.64-1.66)	0.90	NA	NA
Hap5	1.59 (0.78-3.24)	0.20	1.58 (0.79-3.19)	0.20	NA	NA
Hap6	1.27 (0.60-2.68)	0.52	2.16 (0.87-5.37)	0.10	0.64 (0.10-4.00)	0.63
Hap7	0.74 (0.50-1.09)	0.13	0.80 (0.51-1.23)	0.30	1.11 (0.29-4.27)	0.88

[a] From conditional logistic regression, with matching on family, and a variance estimator that incorporates sibling correlation.
[b] NA, data not available

Table 5B. Statistically significant haplotype associations obtained from analysis stratified by high aggressiveness (i. e., high TNM stage or Gleason score) and low aggressiveness (i. e., low TNM stage and Gleason score) [a]

Haplotype	Stratification	All Subjects (n=395...465)		European Americans (n=362...418)		African-Americans (n=33...39)	
		OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value
CYP3A4							
Hap4	Low TNM and grade	0.06 (0.008-0.50)	**0.009**	0.09 (0.01-0.68)	**0.02**	NA [b]	NA
SRD5A2							
Hap3	High TNM or grade	0.52 (0.29-0.91)	**0.02**	0.53 (0.30-0.95)	**0.03**	NA	NA

[a] From conditional logistic regression, with matching on family, and a variance estimator that incorporates sibling correlation.
[b] NA, data not available

Table 6. Annotation of *CYP3A4*, *CYP17* and *SRD5A2* genomic sequences

Gene	Annotation	Base pairs	Sub annotation	Base pairs
CYP3A4	5' region	1-10481		
	Exon 1	10482-10642		
			5' UTR	10482-10571
			Start codon	10572-10574
			Translated region	10572-10642
	Intron 1	10643-14574		
	Exon 2	14575-14668		
	Intron 2	14669-16579		
	Exon 3	16580-16632		
	Intron 3	16633-22072		
	Exon 4	22073-22172		
	Intron 4	22173-24526		
	Exon 5	24527-24640		
	Intron 5	24641-24905		
	Exon 6	24906-24994		
	Intron 6	24995-26259		
	Exon 7	26260-26408		
	Intron 7	26409-27502		
	Exon 8	27503-27630		
	Intron 8	27631-28314		
	Exon 9	28315-28381		
	Intron 9	28382-30736		
	Exon 10	30737-30897		
	Intron 10	30898-32482		
	Exon 11	32483-32709		
	Intron 11	32710-33768		
	Exon 12	33769-33931		
	Intron 12	33932-36520		
	Exon 13	36521-37073		
			Translated region	36521-36613
			Stop codon	36614-36616
			3' UTR	36617-37073
	3' region	37074-39071		

CYP17	5' region	1-9992		
	Exon 1	9993-10337		
			5' UTR	9993-10040
			Start codon	10041-10043
			Translated region	10041-10337
	Intron 1	10338-12009		
	Exon 2	12010-12148		
	Intron 2	12149-12387		
	Exon 3	12388-12617		
	Intron 3	12618-13279		
	Exon 4	13280-13366		
	Intron 4	13367-14193		
	Exon 5	14194-14409		
	Intron 5	14410-14721		
	Exon 6	14722-14891		
	Intron 6	14892-15790		
	Exon 7	15791-15894		
	Intron 7	15895-16416		
	Exon 8	16417-16872		
			Translated region	16417-16697
			Stop codon	16698-16700
			3' UTR	16701-16872
	3' region	16873-26865		
SRD5A2	5' region	1-9995		
	Exon 1	9996-10307		
			5' UTR	9996-10026
			Start codon	10027-10029
			Translated region	10027-10307
	Intron 1	10308-57160		
	Exon 2	57161-57324		
	Intron 2	57325-59454		
	Exon 3	59455-59556		
	Intron 3	59557-61469		
	Exon 4	61470-61620		
	Intron 4	61621-64664		
	Exon 5	64665-66344		
			Translated region	64665-64728
			Stop codon	64729-64731
			3' UTR	64732-66344
	3' region	66345-76341		

What is claimed is:

1. An isolated polynucleotide selected from the group consisting of a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS 1-34.

2. A fragment of said isolated polynucleotide of claim 1, wherein said fragment comprises a polymorphic site in the polymorphic sequence.

3. An isolated polynucleotide comprising a sequence complementary to one or more of the polymorphic sequences (SEQ ID NOS 1-34) of claim 1.

4. A fragment of said complementary nucleotide sequence of claim 3, wherein said fragment comprises a polymorphic site in the polymorphic sequence.

5. The isolated polynucleotide of any of claims 1 to 4, wherein said polynucleotide is DNA, RNA, cDNA, or mRNA.

6. The isolated polynucleotide of any of claims 1 to 5, wherein at least one single nucleotide polymorphism is at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581]

of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33 and position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34.

7. The isolated polynucleotide of claim 6, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19,

[CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33 and [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34.

8. The complement of any of the isolated polynucleotides of claim 7.

9. The isolated polynucleotide of any of claims 1 to 8, wherein the nucleotide comprises part of the *CYP17* gene, the *CYP3A4* gene or the *SRD5A2* gene.

10. A polypeptide encoded by a polynucleotide according to any of claims 1 to 9.

11. An antibody to a polypeptide according to claim 10.

12. The isolated polynucletotide of any of claims 1 to 9, further comprising a detectable label.

13. The isolated polynucleotide of claim 12, wherein said detectable label is selected from the group consisting of fluorophore, radionuclide, peptide, enzyme, antibody and antigen.

14. The isolated polynucleotide of claim 13, wherein said fluorophore is a fluorescent compound is selected from the group consisting of Hoechst

33342, Cy2, Cy3, Cy5, CypHer, coumarin, FITC, DAPI, Alexa 633, DRAQ5 and Alexa 488.

15. A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising analysing a biological sample containing nucleic acid obtained from said subject to detect the presence or absence of one or more single nucleotide polymorphisms at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID

No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

16. The method according to claim 15, wherein said nucleic acid is DNA, RNA, cDNA or mRNA.

17. The method according to claims 15 or 16, wherein said single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27,

[CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44 and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

18. The method according to claims 15 or 16, wherein said single nucleotide polymorphism is selected from the complement of any of the single nucleotide polymorphisms of claim 17.

19. The method of any of claims 15 to 18, wherein said analysis is accomplished by sequencing, genotyping, fragment analysis, hybridisation, restriction fragment analysis, oligonucleotide ligation or allelle specific PCR.

20. The method of claim 19, wherein the analysis is accomplished by hybridisation, the method comprising the steps of

i) contacting said nucleic acid with an oligonucleotide that hybridises to one or more isolated polynucleotide polymorphic sequence selected from the group consisting of SEQ ID NOS 1-36 and SEQ ID NOS 42-45 or its complement;

ii) determining whether the nucleic acid and said oligonucleotide hybridize;

whereby hybridisation of the nucleic acid to the oligonucleotide indicates the presence of the polymorphic site in the nucleic acid.

21. A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, or predicting an individual's response to a drug, said method comprising adding an antibody to a polypeptide present in a biological sample obtained from said subject which polypeptide is encoded by a polynucleotide selected from the group consisting of SEQ ID NOS 1-36 and SEQ ID NOS 42-45, or the complement thereof, and detecting specific binding of said antibody to said polypeptide.

22. A kit comprising at least one isolated polynucleotide of at least 5 contiguous nucleotides of SEQ ID NOS 1-36 or SEQ ID NOS 42-45, or the complement thereof, and containing at least one single nucleotide polymorphic site associated with a disease, condition or disorder related to prostate or breast cancer, together with instructions for the use thereof for detecting the presence or the absence of said at least single nucleotide polymorphism in said nucleic acid.

23. An oligonucleotide array comprising at least one oligonucleotide capable of hybridising to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide comprises a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS 1-36 or SEQ ID NOS 42-45.

24. The oligonucleotide array according to claim 23, wherein said first polynucleotide comprises a fragment of any of said nucleotide sequences, said fragment comprising a polymorphic site in said polymorphic sequence.

25. The oligonucleotide array according to claim 23 wherein the first polynucleotide is a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences of SEQ ID NOS 1-36 or SEQ ID NOS 42-45.

26. The oligonucleotide array according to claim 25, wherein the first polynucleotide comprises a fragment of said complementary sequence, said fragment comprising a polymorphic site in said polymorphic sequence.

27. The kit of claim 22 or the array of any of claims 23 to 26, wherein the position of said polymorphic site is at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID

No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

28. The kit of claim 22 or the array of claim 27, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5'

region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44 and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

29. The kit of claim 28 or the array of claim 27, wherein at least one single nucleotide polymorphism is the complement of any of the single nucleotide polymorphisms of claim 28.

30. The kit of claim 22 or 27 to 29 or the array of any of claims 23 to 29, wherein said oligonucleotide further comprises a detectable label.

31. The kit of claim 30 or the array of claim 30, wherein said label is selected from the group consisting of of fluorophore, radionuclide, peptide, enzyme, antibody or antigen.

32. The kit of claim 30 or the array of claim 30, wherein said fluorophore is a fluorescent compound selected from the group consisting of Hoechst 33342, Cy2, Cy3, Cy5, CypHer, coumarin, FITC, DAPI, Alexa 633 DRAQ5 and Alexa 488.

33. A method of treatment or prophylaxis of a subject comprising the steps of

i) analysing a biological sample containing nucleic acid obtained from said subject to detect the presence or absence of at least one single nucleotide polymorphism in SEQ ID NOS 1-36 or SEQ ID NOS 42-45, or the complement thereof, associated with a disease, condition or disorder related to prostate or breast cancer; and

ii) treating the subject for said disease, condition or disorder if step i) detects the presence of at least one single nucleotide polymorphism

in SEQ ID NOS: 1-36 or SEQ ID NOS 42-45, or the complement thereof.

34. The method of claim 33, wherein said nucleic acid is selected from the group consisting of DNA, RNA and mRNA.

35. The method of claims 33 or 34, wherein the sample is analysed to detect the presence or absence of at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31,

position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

36. The method of claim 35, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base

pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

37. The method of claim 35, wherein at least one single nucleotide polymorphism is the complement of any of the single nucleotide polymorphisms of claim 36.

38. The method of any of claims 33 to 37, wherein said method counteracts the effect of said at least one single nucleotide polymorphism detected.

39. The method of claims 33 to 38, wherein the method comprises treatment with a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS 1-36 and SEQ ID NOS 42-45, or their complement, provided that the polymorphic sequence, or the complement, does not contain at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14,

position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

40. The method of claim 39, wherein the polymorphic sequence does not contain at least one single nucleotide polymorphism selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11,

[CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

41. The method of claim 39, wherein the polymorphic sequence does not contain at least one single nucleotide polymorphism which is the complement of any of the single nucleotide polymorphisms of claim 40.

42. The method of any of claims 33 to 38, wherein said method comprises treatment with a polypeptide which is encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS 1-36 and SEQ ID NOS 42-45 or their complement, provided that the polymorphic sequence, or the complement, does not contain at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position

[CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488] of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44, and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45.

43. The method of claim 42, wherein the polymorphic sequence does not contain at least one single nucleotide polymorphism selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

44. The method of claim 42, wherein the polymorphic sequence does not contain at least one single nucleotide which is the complement of any of the single nucleotide polymorphisms of claim 43.

45. The method of claims 33 to 38, wherein said method comprises treatment with an antibody that binds specifically with a polypeptide encoded by a polynucleotide selected from the group consisting of SEQ ID NOS 1-36 and SEQ ID NOS 42-45, or the complement thereof.

46. A method for predicting the genetic ability of a subject or an organism to metabolise a chemical, said method comprising analysing a biological sample containing nucleic acid obtained from said subject or organism to detect the presence or absence of one or more single nucleotide polymorphisms at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID No. 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID No. 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID No. 3, position [CYP3A4_5' region -747] of SEQ ID No. 4, position [CYP3A4_ IVS7 -202] of SEQ ID No. 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID No. 6, position [CYP3A4_ IVS2 -132] of SEQ ID No. 7, position [CYP3A4_IVS1 -868] of SEQ ID No. 8, position [CYP3A4_5' region -847] of SEQ ID No. 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID No. 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID No. 11, position [CYP3A4_IVS3 +1992] of SEQ ID No. 12, position [CYP3A4_IVS9 +841] of SEQ ID No. 13, position [CYP3A4_IVS12 -473] of SEQ ID No. 14, position [CYP3A4_IVS12 +581] of SEQ ID No. 15, position [CYP3A4_IVS12 +586] of SEQ ID No. 16, position [CYP3A4_IVS12 +646] of SEQ ID No. 17, position [CYP3A4_IVS3 -734] of SEQ ID No. 18, position [CYP17_IVS1 -271] of SEQ ID No. 19, position [CYP17_IVS5 +75] of SEQ ID No. 20, position [CYP17_IVS1 +426] of SEQ ID No. 21, position [CYP17_IVS1 -99] of SEQ ID No. 22, position [CYP17_IVS1 -700] of SEQ ID No. 23, position [CYP17_IVS1 -565] of SEQ ID No. 24, position [CYP17_IVS3 +141] of SEQ ID No. 25, position [CYP17_5' region -1488]

of SEQ ID No. 26, position [CYP17_5' region -1204] of SEQ ID No. 27, position [CYP17_IVS1 +466] of SEQ ID No. 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID No. 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID No. 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID No. 31, position [SRD5A2_5' region -870] of SEQ ID No. 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID No. 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID No. 34, position [SRD5A2_IVS2+626] of SEQ ID No. 35, position [SRD5A2_5' region -8029] of SEQ ID No. 36, position [CYP3A4_IVS7+34] of SEQ ID No. 42, position [CYP3A4_5' region –1232] of SEQ ID No. 43, position [SRD5A2_5' region –3001] of SEQ ID No. 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID No. 45,
wherein the presence of a polymorphism at one or more of said positions is indicative of the subject's or organism's ability or inability to metabolise said chemical.

47. The method of claim 46, wherein said analysis comprises detecting or absence of one or more single nucleotide polymorphisms selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID No. 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID No. 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID No. 3, [CYP3A4_5' region -747C>G] of SEQ ID No. 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID No. 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID No. 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID No. 7, [CYP3A4_IVS1 -868C>T] of SEQ ID No. 8, [CYP3A4_5' region -847A>T] of SEQ ID No. 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID No. 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID No. 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID No. 12, [CYP3A4_IVS9 +841T>G] of SEQ ID No. 13, [CYP3A4_IVS12 -473T>G] of SEQ ID No. 14, [CYP3A4_IVS12 +581C>T] of SEQ ID No. 15, [CYP3A4_IVS12 +586G>A] of SEQ ID No. 16, [CYP3A4_IVS12 +646C>A] of SEQ ID No. 17, [CYP3A4_IVS3 -734G>A] of SEQ ID No. 18, [CYP17_IVS1 -271A>C] of

SEQ ID No. 19, [CYP17_IVS5 +75C>G] of SEQ ID No. 20, [CYP17_IVS1 +426G>A] of SEQ ID No. 21, [CYP17_IVS1 -99C>T] of SEQ ID No. 22, [CYP17_IVS1 -700C>G] of SEQ ID No. 23, [CYP17_IVS1 -565G>A] of SEQ ID No. 24, [CYP17_IVS3 +141A>T] of SEQ ID No. 25, [CYP17_5' region -1488C>G] of SEQ ID No. 26, [CYP17_5' region -1204C>T] of SEQ ID No. 27, [CYP17_IVS1 +466G>A] of SEQ ID No. 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID No. 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID No. 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID No. 31, [SRD5A2_5' region -870G>A] of SEQ ID No. 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID No. 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID No. 34, [SRD5A2_IVS2+626C>T] of SEQ ID No. 35, and [SRD5A2_5' region -8029C>T] of SEQ ID No. 36, [CYP3A4_IVS7+34T>G] of SEQ ID No. 42, [CYP3A4_5' region –1232C>T] of SEQ ID No. 43, [SRD5A2_5' region –3001G>A] of SEQ ID No. 44, [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID No. 45.

48. The method of either of claims 46 or 47, wherein the method further comprises predicting the response of the subject to the chemical by their ability or inability to metabolise the chemical.

49. The method according to any of claims 46 to 48, wherein said chemical is a drug or a xenobiotic.

50. The method according to any of claims 46 to 49, wherein said organism is selected from the group consisting of bacterium, fungus, protozoa, alga, fish, plant, insect and mammal.

51. A vector comprising a polynucleotide selected from the group consisting of a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID NOS 1-36 or SEQ ID NOS 42-45.

52. A host cell transformed with the vector of claim 51.

53. The host cell of claim 52, wherein said host cell is selected from the group consisting of bacterium, fungus, protozoa, alga, fish, plant, insect and mammal.

54. The host cell of claim 53, wherein said mammal cell is a human cell.

55. Method of metabolising a chemical using the host cell of either of claims 52 or 53.

56. Method for making a host cell resistant to a chemical, said method comprising transforming said cell with any of the polynucleotides of claims 1 to 9 or with any of the vectors of claim 51.

57. An isolated haplotype selected from the group consisting of CYP3A4_Hap4 and SRD52_Hap3.

58. The isolated CYP3A4_Hap4 haplotype of Claim 57 wherein said haplotype comprises Allele T at [CYP3A4_5' region –1232C>T], Allele C at [CYP3A4_5' region –747C>G], Allele G at [CYP3A4_5' region –392A>G], Allele G at [CYP3A4_IVS7+34T>G], Allele T at [CYP3A4_IVS7-202C>T], Allele G at [CYP3A4_stop+766T>G], Allele C at [CYP3A4_stop+1454C>T], Allele T at [CYP3A4_stop+1639A>T] and Allele C at [CYP3A4_stop+2204G>C].

59. The isolated SRD52_Hap3 haplotype of Claim 57 wherein said haplotype comprises Allele C at [SRD5A2_5' region –8029C>T], Allele G at [SRD5A2_5' region –3001G>A], Allele G at [SRD5A2_145G>A], Allele G at [SRD5A2_265G>C], Allele T at [SRD5A2_IVS2+626C>T], Allele G at [SRD5A2_stop+1552G>A], Allele G at [SRD5A2_stop+3059G>A] and Allele G at [SRD5A2_stop+9301G>C].

60. A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising analysing a biological sample obtained from said subject to detect the presence or absence of a haplotype as defined in any of claims 57-59.

61. A method of diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising adding an antibody to a polypeptide present in a sample obtained from said subject which polypeptide is encoded by a haplotype as defined in any of claims 57-59, or the complement thereof, and detecting specific binding of said antibody to said polypeptide.

62. A method of treatment or prophylaxis of a subject comprising the steps of
i) analysing a sample of biological material containing a nucleic acid obtained from said subject to detect the presence or absence of at least one haplotype as defined in any of claims 57-59, or the complement thereof, associated with a disease, condition or disorder related to prostate or breast cancer; and
ii) treating the subject for said disease, condition or disorder if step i) detects the presence of at least one said haplotype, or the complement thereof.

63. The method of claim 62 wherein the method comprises treatment with a portion of the isolated CYP3A4_Hap4 haplotype according to claim 58 wherein said portion of said haplotype does not consist of at least one allele from the group consisting of Allele T at [CYP3A4_5' region –1232C>T], Allele C at [CYP3A4_5' region –747C>G], Allele G at [CYP3A4_5' region –392A>G], Allele G at [CYP3A4_IVS7+34T>G], Allele T at [CYP3A4_IVS7-202C>T], Allele G at [CYP3A4_stop+766T>G], Allele C at [CYP3A4_stop+1454C>T], Allele T at [CYP3A4_stop+1639A>T] and Allele C at [CYP3A4_stop+2204G>C].

64. The method of claim 62 wherein the method comprises treatment with a portion of the isolated SRD5A2_Hap3 haplotype of Claim 59 wherein said portion of said haplotype does not comprise of at least one allele from the group consisting of Allele C at [SRD5A2_5' region –8029C>T], Allele G at [SRD5A2_5' region –3001G>A], Allele G at [SRD5A2_145G>A], Allele G at [SRD5A2_265G>C], Allele T at [SRD5A2_IVS2+626C>T], Allele G at [SRD5A2_stop+1552G>A], Allele G at [SRD5A2_stop+3059G>A] and Allele G at [SRD5A2_stop+9301G>C].

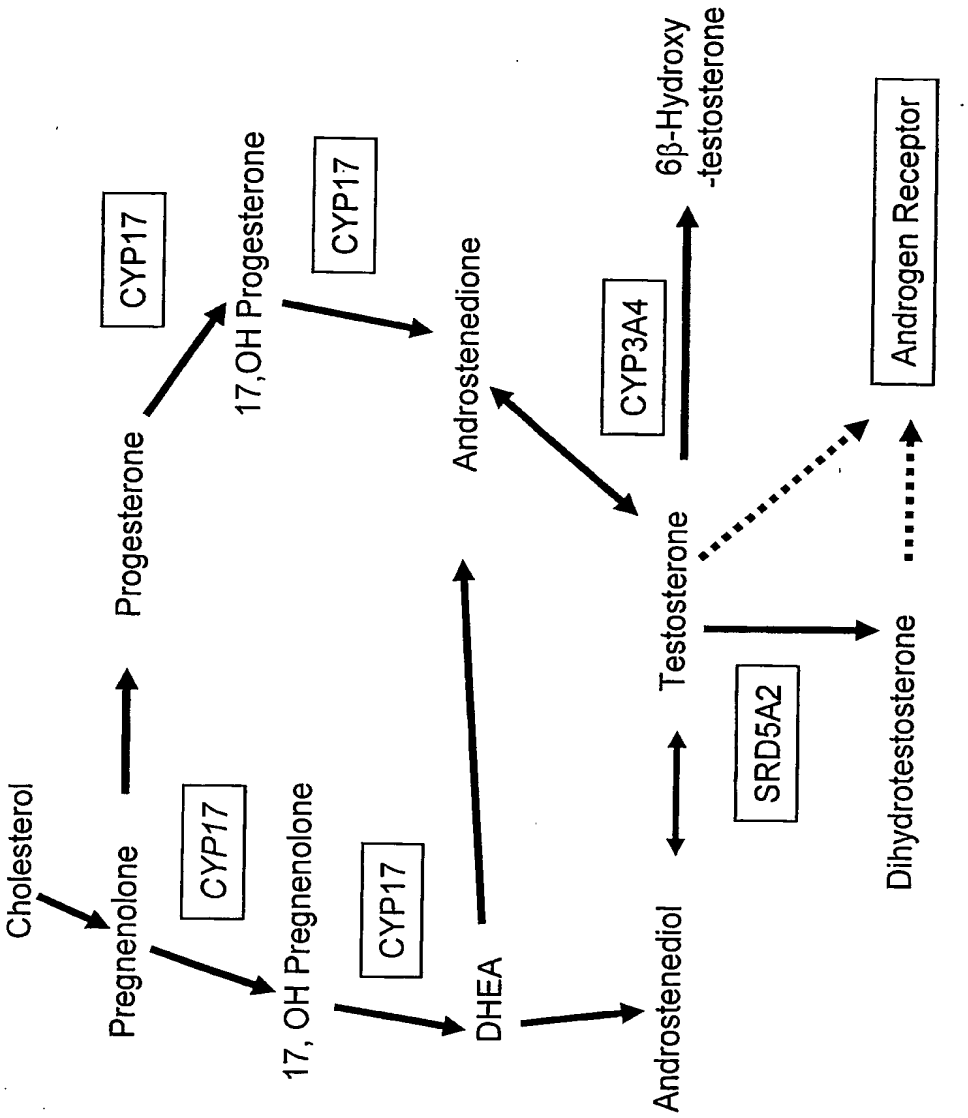
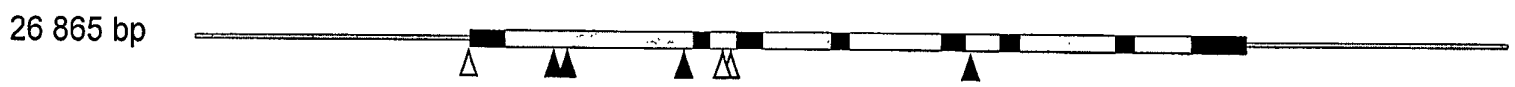
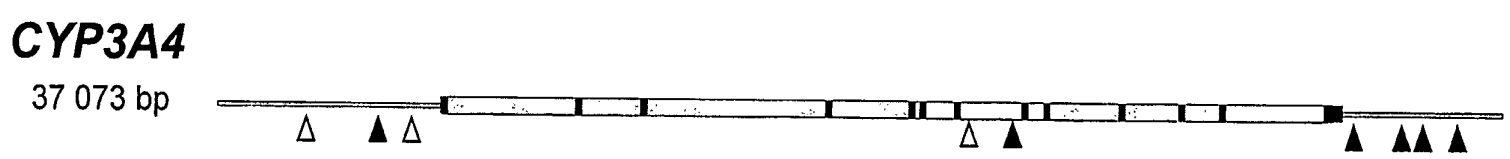


Figure 1: Testosterone biosynthetic pathway



	SNP29: -34T>C	SNP04: IVS1 +426G>A	SNP20: IVS1 +466G>A	SNP06: IVS1 -99C>T	SNP07: IVS2 +105A>C	SNP22: IVS2 -83C>T	SNP03: IVS5 +75C>G	Frequency (all)		Frequency (EA)		Frequency (AA)	
								Controls	Cases	Controls	Cases	Controls	Cases
Hap1	T	C	C	C	A	C	C	547 (.57)	527 (.60)	494 (.57)	475 (.60)	50 (.66)	47 (.62)
Hap2	C	T	.	T	C	.	G	259 (.27)	216 (.25)	253 (.29)	208 (.26)	5 (.07)	6 (.08)
Hap3	C	T	.	.	.	.	G	91 (.09)	86 (.10)	85 (.10)	79 (.10)	3 (.04)	7 (.09)
Hap4	Composite							63 (.07)	51 (.06)	42 (.05)	32 (.04)	18 (.24)	16 (.21)

Figure 2A

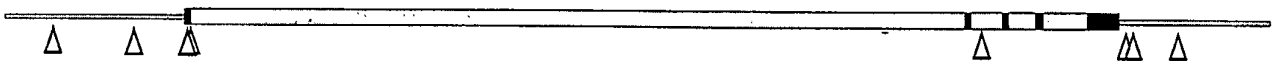


	SNP47: -1232C>T	SNP12: -747C>G	SNP11: -392A>G	SNP01: IVS7 +34T>G	SNP13: IVS7 -202C>T	SNP24: stop +766 delT	SNP25: stop +1454C>T	SNP05: stop +1639A>T	SNP15: stop +2204G>C	Frequency (all) Controls	Frequency (all) Cases	Frequency (EA) Controls	Frequency (EA) Cases	Frequency (AA) Controls	Frequency (AA) Cases
Hap1	C	C	A	T	C	T	C	A	G	651 (.68)	596 (.68)	629 (.72)	577 (.73)	16 (.21)	13 (.17)
Hap2	.	G	.	.	.	.	.	.	.	65 (.07)	62 (.07)	64 (.07)	59 (.07)	1 (.01)	2 (.03)
Hap3	.	.	.	.	T	G	.	T	C	63 (.07)	64 (.07)	59 (.07)	58 (.07)	4 (.05)	6 (.08)
Hap4	T	.	G	G	T	G	.	T	C	45 (.05)	25 (.03)	34 (.04)	19 (.02)	10 (.13)	5 (.07)
Hap5	Composite									136 (.14)	133(.15)	88 (.10)	81 (.10)	45 (.59)	50 (.66)

Figure 2B

SRD5A2

76 341 bp



	SNP17: - 8029C>T	SNP26: - 3001G>A	SNP22: A49T (145G>A)	SNP20: V89L (265G>C)	SNP12: IVS2 + 626C>T	SNP01: stop + 1552G>A	SNP13: stop + 3059G>A	SNP15: stop + 9301G>C	Frequency (all)		Frequency (EA)		Frequency (AA)	
									Controls	Cases	Controls	Cases	Controls	Cases
Hap1	T	G	G	G	C	G	G	G	376 (.39)	348 (.40)	352 (.40)	321 (.40)	19 (.25)	20 (.26)
Hap2	C	A	.	C	T	.	.	C	218 (.23)	212 (.24)	206 (.24)	197 (.25)	11 (.14)	13 (.17)
Hap3	C	.	.	.	T	.	.	.	108 (.11)	84 (.10)	102 (.12)	81 (.10)	6 (.08)	3 (.04)
Hap4	C	.	.	.	.	A	A	.	73 (.08)	73 (.08)	70 (.08)	65 (.08)	-	7 (.09)
Hap5	C	A	.	C	T	.	.	.	41 (.04)	42 (.05)	41 (.05)	42 (.05)	-	-
Hap6	C	.	.	.	.	.	.	.	32 (.03)	27 (.03)	19 (.02)	20 (.03)	13 (.17)	7 (.09)
Hap7	Composite								112 (.12)	94 (.10)	84 (.10)	68 (.09)	27 (.36)	26 (.34)

Figure 2C

pto_PB0262.txt
SEQUENCE LISTING

<110> Loukola, Anu-Maria
Penn, Sharron G.
Rank, David R.
Hanzel, David K.
Casey, Graham.
Witte, John S.

<120> Detection Methods

<130> PB0262

<140> to be assigned
<141> 2003-09-25

<150> US 60/413,583
<151> 2002-09-25

<150> US 60/491,842
<151> 2003-08-01

<160> 45

<170> PatentIn version 3.1

<210> 1
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: G.

<400> 1
atgagaattt ctgccacata gcagaacgac acatgtttga atgttataag tggtagttgg 60

aggcactttc tagaggcatg caggcataga tagccatgtt ctaagagtaa agggcaaccc 120

taagcaaacc tggcatgcta gaaagtcagt ctgcggtctg tggatcacct acatcagatc 180

aaatgccaat tctcagcctc c 201

<210> 2
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 2
tgatagaagc caggcttctc acctttgcag aagggagtca tggattcaga aagggagaaa 60

actagcatga atcctatgaa attagattgg aatggatgta accgtgtata ttcataccct 120

tgtagataga tagatgggta gatagatgat agataggtaa cagatagatg acagataatg 180

agatagatag atgtaaatgt a 201

<210> 3
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 3
ggcaggagaa tcacttgaac ctgggaggcg gatgttgaag tgagctgaga ttgcaccact 60

gcactccagt ctgggtgaga gtgagactca gtcttaaaaa aatatgcctt tttgaagcac 120

gtacattttg taacaaagaa ctgaagctct tattatatta ttagttttga tttaatgttt 180

tcagcccatc tcctttcata t 201

<210> 4
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: G.

<400> 4
aagtcaccag aaagtcagaa gggatgacat gcagaggccc agcaatctca gctaagtcaa 60

ctccaccagc ctttctagtt gcccactgtg tgtacagcac cctggtaggg accagagcca 120

tgacagggaa taagactaga ctatgccctt gaggagctca cctctgttca gggaaacagg 180

cgtggaaaca caatggtggt a 201

<210> 5
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 5
ctgtagtcca atagataaag gcaaagagat tagggcattg aattttgttc cttttatcct 60

tcaaaagatg cacaaggggc tgctgatctc actgctgtag cggtgctcct tatgcataga 120

cctgcccttg ctcagccact ggcctgaaag aggggcaaaa gtcatagaag gaatggcttc 180

cagttgagaa ccttgatgtc t 201

<210> 6
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: C.

<400> 6
gaactattgg aactgataaa cacattcagt aaagttgcag gatacaaaat cagcatacaa 60

aaatcagtag catttctata tgccaatagt gaacaatctg gcaaaaataa aaaagtaatc 120

ccatttacaa tagccacaaa taaaactaaa tacctagaaa ttaacttaat caaagaagag 180

aaaggtctct acaatgaata c 201

<210> 7
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 7
ataagtcatt cagtatccac aacacttgga gagaattcaa gagtgatttt aaatttccct 60

tttcaaatac ctcctctgtt ttctcttatt tcctttatga cgtctccaaa taagcttcct 120

ctaactgcca gcaagtctga tttcattggc ttcgactgtt ttcatcccaa ttagaggcag 180

ggttaagtac attaaaaata a 201

<210> 8
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (104)..(104)
<223> Alternative allele: T.

<400> 8
aactgcccct aggatccaat catctcctac caggccccac ctccagtatt ggggattgca 60

tttcaacatg agattttggt aggggcacag attcagacca tatcactggc actgtgctaa 120

tcagatgaat atcaccagtt ggaaggctag attccacaag aggaggaatg acctggaaat 180

tggttcttta gttgtgattc t 201

<210> 9
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (100)..(100)
<223> Alternative allele: T.

<400> 9
ggggtcccct tgccaacaga atcacagagg accagcctga aagtgcagag acagcagctg 60

aggcacagcc aagagctctg gctgtattaa tgacctaaga agtcaccaga aagtcagaag 120

ggatgacatg cagaggccca gcaatctcag ctaagtcaac tccaccagcc tttctagttg 180

cccactgtgt gtacagcacc c 201

<210> 10
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: base deleted.

<400> 10
tcaggcacag tggctcacgc ctgtaatcct agcagtttgg gaggctgagc cgggtggatc 60

gcctgaggtc aggagttcaa gacaagcctg gcctacatgg ttgaaacccc atctctacta 120

aaaatacaca aattagctag gcatggtgga ctcgcctgta atctcactac acaggaggct 180

gaggcaggag aatcacttga a 201

<210> 11
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 11
tgggtgtggg agtccaagca agcagagaag gggtcgacgc agaggggtgg cttgcaagag 60

cagccagagc ctaaataggg tatggagaac ccacatgagg cgaggagggc atccatgagt 120

gggaggggtt gggtgaggtt tggctacata aaggggattg atcaaataag taaatgtatt 180

aaggatgata gaagccaggc t 201

<210> 12
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: C.

<400> 12
ttgcatttct ctaatgacca gtgatgatga gcatttttc acatgtctgt tggctgcata 60

gatgtcttct tttgagaagt gtctgttcat atcctttgcc tatttttga tggggttgtt 120

tgctttttt cttgtaaatt tgtttaagtt ctttgtagat tctggatgtt agcccttcgt 180

cagatggata gattgcaaaa a 201

<210> 13
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: G.

<400> 13
taactattgg ttctagagag caggactggg cttactccag catactgctt taaatatatc 60

catgtctaca tccacttttg tctgtatgtc tatgtatcta tctatgtatc tatctagcta 120

tgtatctatc tatctatcta tctatcatct atctatctat ctatcatcta tccatctatc 180

atctatcatt tatccatcta t 201

<210> 14
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: G.

<400> 14
cttcccatct ttacactgga tgggttcaat tgggaggaat tactggactc tggaagttga 60

agactgtcca tataattaaa atgtacaata actacccagg tttaccttgc aagtttcaac 120

atacacaaaa ttaactttat atgactcttc aaaaacagtt tgccatcata cctaataatc 180

tggtttaaat tttaaaaact c 201

<210> 15
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 15
tgcccagagt gtggctttaa aagcttcccc attgcttctc atgtgaagcc aaggttgaga 60

atgactaatt taaggcattt ctggtggata taaaggacta ccacagtcca aggccatcct 120

gactgacctc accttccagg tgcctagctc catccagctg ggctcctttt caacccaatt 180

ataactctat taatgttgtt c 201

<210> 16
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: A.

<400> 16
agagtgtggc tttaaaagct tccccattgc ttctcatgtg aagccaaggt tgagaatgac 60

taatttaagg catttctggt ggatataaag gactaccaca gtccaaggcc atcctgactg 120

acctcacctt ccaggtgcct agctccatcc agctgggctc cttttcaacc caattataac 180

tctattaatg ttgttcccag c 201

<210> 17
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: A.

<400> 17
taatttaagg catttctggt ggatataaag gactaccaca gtccaaggcc atcctgactg 60

acctcacctt ccaggtgcct agctccatcc agctgggctc cttttcaacc caattataac 120

tctattaatg ttgttcccag ccaggcatgg tggctcatgc ctgtaatccc agcactttgg 180

gaggccgaag caggcggatc a 201

<210> 18

<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: A.

<400> 18
ctaatttgat tgcactgtgg tctgagagac agtttgttat gatttctgtt cttttacatt 60

tgctgaggag tgctttactt ccaattatgt ggtcaatttt ggaataagtg cgatgtggtg 120

ctgagaagaa tgtatattct gttgatttgg ggtggagagt tctgtagatg tctattaggt 180

ccgcttggtg cagagctgag t 201

<210> 19
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (100)..(100)
<223> Alternative allele: C.

<400> 19
ggacaggcat agtttagaga gtttatccca tccagagttg ccttctgtgg tcagaaactg 60

atgagcaaaa agaagcccag agggcaccct gtcagcgaaa agaaccccaa tgctgctgca 120

ttctaattaa gggttctttc tttctccttg atctactgta tttctgaagg aattgggagt 180

aggaggcctt agggtctgtc 200

<210> 20
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: G.

<400> 20
tggccttcct gctgcacaat cctcaggtgt gcttcccct cattgatcct agaccccagc 60

cagcccaatc tctgggctcc agagaaaggg agagccaatt ctctcaggct ttctgtgcag 120

gaagactagg cctgccctgc tccttaccca agcagtagtt ggctttgacc ccagagtaga 180

gctgccccat cttctggaag c 201

<210> 21
<211> 201

<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: A.

<400> 21
cagcacttag cctagcaccc agcacagtaa gtgcccctta tacagccagg attcatgtta 60

cttttcatgg aaaatggggg cagtgactac tgtcctccat gaaagctgct ggggagaatt 120

agcctagcta ttgcaggctg ggattgctgc tttcctggtg ctatttccag ctactcaggc 180

tcacaggggc agttttctac a 201

<210> 22
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 22
attgggagta ggaggcctta gggtctgtcc taccaagtcc ttgcagtcat ggtggagtgc 60

agtggggctg tgcccacatg ggagtcagca tgccaggtac ctgccttctc ctccaggaag 120

gaaagcaggg accagaggtg taagggcaag agtggggtgg atggtgtgag attcctacag 180

ccttgcctgc tctctaaagg c 201

<210> 23
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: G.

<400> 23
gccactgtgc cctgccagcc tctcagcttt gatcaagcca agggttggtt tatttttct 60

tggaccaatc agccaggtct gctgaccaac tacctagctc ccacctctgc tggcttcctc 120

ccgggggcag agaagatgga gaaggctagt catgtggatc ttcagggtca ggaaatggaa 180

aagggaggct ttggaccctt t 201

<210> 24
<211> 201
<212> DNA

<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: A.

<400> 24
atggagaagg ctagtcatgt ggatcttcag ggtcaggaaa tggaaaaggg aggctttgga 60

ccctttttgct ttgggggggca cctctaggag gaggcagctc ggcccaagtc cagactgggt 120

agacaaaaca tctgcactct ccaaatgtgg gcttgtggct gggtatgcag gcttgcaatg 180

gaagggtaaa cctgagtgag g 201

<210> 25
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 25
ctgacattgt ccccaatctt ccttcctttt tacttccctg ctccagccgc aatgacccat 60

ctttttcctg attacctccg ccacctctac ctcctctgcc acttaaaacc tttgccattt 120

ctctgcagag atagatttag ccttttaatt atgcacctta gtactccaga taatgacctt 180

catttctttt ccaattacca t 201

<210> 26
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (100)..(100)
<223> Alternative allele: G.

<400> 26
atttttaggg aacaagggaa aacaaccata aggtctgact gcctgcaggg tcgggcagaa 60

agagccatat tttccttctt gagagaggct ataaatggac atgcaagtag ggaagatatc 120

actaaattct tttcctagca aggagtatta ttattaatac cctgggaaag gaatgcattc 180

ctgggggggag gtctataaac a 201

<210> 27
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<400> 27
tagggtgggg aaaaactccg ccctggtaaa tttgtggtca gaccggttct ctgctgtcga 60

accctgtttg ctgttgttta aggtgtttat caagacagta cgtgcaccgc tgaacataga 120

ccctcatctg tagttctgct tttgcccttt gccttgtgat ctttgttgga cccttatcag 180

tggttctgct tttgcccttt g 201

<210> 28
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: A.

<400> 28
tacagccagg attcatgtta cttttcatgg aaaatggggg cagtgactac tgtcctccat 60

aaaagctgct ggggagaatt agcctagcta ttgcaggctg ggattgctgc tttcctggtg 120

ctatttccag ctactcaggc tcacaggggc agttttctac aatgacattt cagggttgct 180

gatgagcctc ccactcagca g 201

<210> 29
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: A.

<400> 29
ctggaggatt ttaagtatgt aagtggaaca atctgttttt ttgtttttgt ttttgtttga 60

gaaggagttt cgctcttgtt gccctggctg gagtgcaatg gcatgatctt ggctcactgc 120

aacccctgcc tcctgagttc aagtgattct cctgcctcag cctccaaaat agctgggatt 180

gcaggcgtgt gccaccatgc c 201

<210> 30
<211> 150
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (50)..(50)
<223> Alternative allele: C.

<400> 30
tcttgtgaag gggtcacccc agcatgagtg ctgagatatg gactctctaa ggaaggggcc 60

gaacgcttgt aattggaata catggaaata tttgtcttct caggcctatg tttgcggaat 120

gcattgtcaa tatttagcaa actgttttga 150

<210> 31
<211> 151
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (51)..(51)
<223> Alternative allele: G.

<400> 31
cgagaacagt tttacaatag acattgcaaa ctctcatgtt tttggaaact agtggcaata 60

tccaaataat gagtagtgta aaacaaagag aattaatgat gaggttacat gctgcttgcc 120

tccaccagat gtccacaaca atatgaagta c 151

<210> 32
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: A.

<400> 32
gtctgcgtgt atgacggcta gacaggagtt cagagaacag cggggtcgcc aggccaccac 60

ctgatgggcc acggctcatt ggctctagga gctgggaaag ggcatcccag gaaagaagcc 120

ctagacttta gcctgagtct gggccactct aggggaccgg gagtggggtg gcgggagagg 180

acgcgcagaa tctcgacttc t 201

<210> 33
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(107)
<223> Alternative allele: eight A's instead of seven after base 100.

<400> 33
agctaattgt tataatagtg gagaaaagat catgaggaca aaaagtgggc agagtcggaa 60

gaaaagagag gaagaaattg agacagaaga catttcattt aaaaaaatat tccattgagc 120

tgggtttgaa atagtgcact gcctgttctc ctaatgctgt atggtgtcat gaaatctatt 180

gtttactgag tctatgagcc 200

<210> 34
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: C.

<400> 34
aactctgaag ccacaaagac ccagagcaaa cccactccca aatgaaaacc ccagtcatgg 60

cttccttttt cttggttaat taggaaagat gagaaattat taggtagacc ttgaatacag 120

gagccctctc ctcatagtgc tgaaaagata ctgatgcatt gacctcattt caaatttgtg 180

cagtgtctta gttgatgagt g 201

<210> 35
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: T.

<300>
<308> NCBI SNP CLUSTER ID: rs413836
<309> 2003-03-07

<400> 35
aaagaaacat tgtttcttaa aacaatgttt taagaaagtg tacgaatttg tgtcaggcca 60

catccaaaac tgtcctgggc tgcatgtggc ccacaggctg cgggttggac aagcctggcc 120

tagaaggctt tgcccccatg tattcatggg ggttggttcc tcactttatt tagttcccta 180

ccaatttgca cctcctcaaa gggactttcc c 211

<210> 36
<211> 213
<212> DNA
<213> Homo sapiens

<220>
<221> SNP

<222> (123)..(123)
<223> Alternative allele: T.

<300>
<308> NCBI SNP CLUSTER ID: rs545303
<309> 2003-03-07

<400> 36
gggaactcac agttttttgg ctgtctcata gagtttgcaa cagtaaaact gcttctttca 60

aagggtctgt gaattctttc agttttcctg gtatgttccc atggtagttc ttgcagcaaa 120

agctcacagt gtgagtctcc acacactgtt ctgtccattc caagcaggag ctgcatgtta 180

gttctgtctg ctatccacca ttttccaatt ttg 213

<210> 37
<211> 20
<212> DNA
<213> Homo sapiens

<400> 37
tggccttgta cgtcgcgaag 20

<210> 38
<211> 21
<212> DNA
<213> Homo sapiens

<400> 38
agcagggcag tgcgctgcac t 21

<210> 39
<211> 39071
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (37334)..(37334)
<223> Unknown base.

<300>
<308> http://www.genome.utah.edu/genesnps/
<309> 2002-06-05
<313> (1)..(37073)

<400> 39
ggatccctac tcactgtctt ctctctacag aacgagatgt ctctggagtc catagaaagc 60

ccaggagcct ggctgggcac ggtggctcct gcctgtaatc ccagcacttt gggaggccga 120

ggcaggcaga tcacctgagc tcaggagttc aagaccagcc tgggcaacat ggcaaaaccc 180

catctctact aaaaatacaa aaaattagct gggcgtggtg gtgcatgcct ctaatcccag 240

ctacttggga ggctgaggca caagaattgc ttgagcccag gaggcagcag ttgcagtgag 300

ctgagattgt gccagtgcac tccagcctgg gcaacagagc aagattccat ttcaaaaaca 360

aaaacaaaca caaacaaaca aacaaaaata gaaagcccag ggaccacctg cgtcaggttc 420

ccagccacac ctttttcttg tcctcctctg tctctggcat cttctcacag gttcctaatt 480

gtttgtggtt gcacaaattc aaaatcccag aaaaattacc acttcacacc cactcagatg 540

gctatttttt ttttgaagga agataacaag tgttgacaag aacatggaga aattggaatt 600

ctcacccatt gctggtgaga atgtaatacg gtgctgctgc tatggaaaac agcttggagt 660

ttcctcaaaa agttcaacag aatttcaatg tgacccagca attcccctct aagttataga 720

tctgagagga ttaaaaacag ttactaaaat acacggactc acatatttct aacagtccaa 780

ttcacaaggg ccaaaaggtg ctaatagccc acatgtccat cgatggatgg ataaataaat 840

tgtggtctat ccatacaatg gaatattatt cggccataaa tggaatgaag tactgacgca 900

tgctacagaa tggatgaacc gcaaaaaaaa tggatgaaca catgctacag aatggatagc 960

ctcactttac tatgaagtga aggccagaaa cgaagtccat atattgcatc atacaaaata 1020

tccagaagag ggaagcccac agagacagaa tgtgcaatgg tggatgccag ggtctgggga 1080

gaggggagag tggggagaaa ctgctcaact ggtacaggct ttattttgga atgatgggaa 1140

cattttgcaa ctagatagag gtagtgattg cagaacacag aatgtactga attccactga 1200

ttttttttcac cttaaaatgg ttaattttca gtcctgagat tggataatca taaaaaaatg 1260

gttaatttta tgttatgtga atttcatccc tatacatatt ttaaacctca gaaatataca 1320

ctagcaggca tggaacaggt cactgtggtg cctgccaagc ccggtgatgt tatctggggt 1380

ccccggccag ccttaagcct cttgctgacc ggtggagggc agaacctttg ccctaaaagt 1440

ataatatcca catgctggca tgattcctgg ccagatggct tctttattag cagtaattga 1500

aactgcctcg atacagacac tgtaccttgc aaccaaaaaa tgactcaaca atgataataa 1560

gggttaagct gggcctttct ctctttgcca gttaaattat atttattata gcttgacatg 1620

aaaaacaaag caactccaac aggtatcaca agggcaaagg acatgaacat tttatcaaag 1680

aagaaatgca gctgtcaaaa atacagaaat attcaacctt gttcataata aagtggctgg 1740

gctcagtggt tcatgcctgt aatcccagtg ctttgcaagg ctgagacagg aggatcattt 1800

gaagccagaa gttcaagacc atcctaggca agtcagttca ataccagact tcatgtctac 1860

aaaacatcaa aaaattagcc aggcatggtg atgcatgcct gttgtcccag ctactcagga 1920

ggctgaggca ggagaattgc ttgagcctgg gaggctgcgg tggcggtgag ccatgattgt 1980

gccattgtac tccagcctgg gcaatgcagc aagactgtct aaataacaaa aataatagta 2040

aagaaaagga ttgggatgcc atttacttgc gtattcaata cacagagtta aaagtaattt 2100

ctacgttttc tatttttta ttactaaaaa aagctggacc attctcacag cctgaaatgc 2160

ttctcacttt cccttcttct gtccaaacac ttctctatga taatgcaaac agtcactcct 2220

ttaggaagac ttcaccccag gtagttccag atcccttat ctctgccttc ccagaactcc 2280

tggtgtctct ccagttccct ccgtgtggtg aagtacccta cctagggttt cagtatggct 2340

ctgtctgcaa aggtcttgtt cacaccttcc cttatggttc tgttgccctg tgttgtgtca 2400

tagcacaggg cacagtggag aacccattca cactgataga gagggcccca tggtcctgga 2460

gataaccatg taaccgatca gaataaggca ttgagggctg ggtgtcaggc gtgggctgca 2520

cttgggtggg caggtcccct ggaaagtcac tgggtttggc aagcttccta gtaacatgtc 2580

tctctggggt ccccccttgga acttcatgca aaaatgctgg ttgctggttt attctagaga 2640

gatggttcat tcctttcatt tgattatcaa agaaactcat gtcccaatta aaggtcataa 2700

agcccagttt gtaaactgag atgatctcag ctgaatgaac ttgctgaccc tctgctttcc 2760

tccagcctct cggtgccctt gaaatcatgt cggttcaagc agcctcatga ggcattacaa 2820

agtttaatta tttcagtgat tattaaacct tgtcctgtgt tgaccccagg tgaatcacaa 2880

gctgaacttc tgacaagaac aagctatcat attcttttca attacagaaa aaagtaagtt 2940

aattgatagg attttttttg tttaaaaaaa atgttactag ttttgaaaag gtaatatgtg 3000

cacatggtaa acactaagaa ggtataagag cataatgctt ttatactact aagaataatg 3060

ttttctctaa gtttttttg gtagatgctt tcatcagatt aagaaaattc cctgctatta 3120

gttgttgaag gtttttatat cataaatgaa agttgaatat tattatcata tattattaat 3180

atattgttat tgaactatca aagccttttc ctaaaaccat tgagatgatc ttataaccat 3240

tctcctttaa cctgttgacg agatcattgg tatttatact atttctctgt taaccattct 3300

tgagtctcag gtttaaattc aacttggtca tggtgtgtca tctttgatca ttgctgtctg 3360

tggcttgcta ctgttttgtt taggattttt gcactgatgc tcatcaatga gactggcatg 3420

ccatcttcct ttgcagtcct gatttttttc tgatttggat catgtggtta tggccctcat 3480

ggaatgagtt gggcatgatg cctttttttc atgtctctgg attgatggga cactttggat 3540

tctctccaga tggccctcaa tggtccctgc ctcctcattg ttaggcccct gggcaagccc 3600

ttctcatttc tggtaggccc aggaacctgt gggggttttg tttgtttgtt tgtttcttga 3660

gtcggagtct cactctgtca cccaggctgg agttggagtg caatggcccg atcttggctc 3720

actgcaacct ccacctccca gattcaagca attctcctgc ctcagcctcc tgagtagctg 3780

gaattacagg cacccaccga cacaccctgc taatttttgt atttttagta cagatggggt 3840

ttcacaatat tggccaagct ggtctcgaac tcctgatctc atgatctgcc cggcttggcc 3900

tcccaaagtg ttgagattac aagcatgagc caccacaccc agtgaacctg tggtttttag 3960

aagctcccca tgcatgtgaa tgctgtgagc atcccaggat gacagccact gtgtgttcag 4020

ctgttggaac tgtgagaaag caccagtggg accttctcca gcacctgcct gctgagttca 4080

tggaagaggc ttgttgggga gatgatgccc tggctgactc ctgaaggatg gttaggaatg 4140

caccagatgg aagctgggtt ggacccactc tatgctgaag aacagcttgt gtggacacaa 4200

ggagacacgg atatgtcatt tttgtagagc ctgaggagtg tccaatcaca ccatttgctt 4260

aaaacatcat gcacacttgg aaaagtggac tgagaccgaa tgaagaagct aacagtggcc 4320

agatcagaaa gggtcttgtg ttacttccta gagatactta gattttatcc tgtgggtgat 4380

aggagcagtt ggagggactg aagacaagga aagaaacatg tttcaagatc tatgtttttc 4440

aagacgcttt tctggtggct gagtagggaa ttccctggat aagtcctgcc cagggtcagg 4500

caaaacaagt taggggggtta ctgaaataag gagtatgaga aatggtgtag gttgtgctga 4560

cgttttgtaa cacatctcat gatgatcttc atttccttca ctaatttcct gtttcattaa 4620

ttcccttcca cgtgctcttc tgaaatttgc ctcacattct ctgatttctc ttttacctgt 4680

tggtttcatc acctttttact ttttgctttc ctggaaacac aaatgattct gattgtgaca 4740

tgtcagaatt atttgcaaca tttgcctttc tgctgaaacc atgagttcac tgaatacaca 4800

atttagtaaa gtgtaggatg cacatgtcgt tttcgtggtc acaaccagct ctgtagcatt 4860

ttataactac actggcagtg tgctgggagg tgtagagaga aatatttatc acatgtgtgg 4920

ctgacacaac ctgccaagtt attttaggag cctccttgga atcccagcaa gaatgctacc 4980

ggcacaattt gtaatcacag catcctgctc catgccttgg cttcatggca tagtcacttc 5040

tgcaagtctc tttccagctg tctgttccca tgtctataaa gtatgagtta aatcatccta 5100

acactactca tcttacaaag ttttcttgct gatgttaaga gagttgggaa agaactgtat 5160

aaactgtgaa gtgccatgga gatgttagtg gttactttat caagaaatag acactctaga 5220

atggagtaga aagccaacag ttatgattga gtcctcctcc tcttcttctt tttattaatt 5280

tataaagaaa agaggtttaa ttgactcaca gttccatatg gctggggagg cctcgggaaa 5340

ctctcagtca tagcaggagg caaaggggaa gaaggcacct tcttcacaag gcggcaggag 5400

agagagagct cctgttcttt tttgtcataa agtctacaga agtgcttata cttcaggaca 5460

agggcaggca gagagaagga aggacattgc ttcaccccag ccctcactga cgagtttgct 5520

aggggacctc actttgtccc agagtagggc agaactctgg ccactaccca ttcagaaggc 5580

ctgggctgca ctgctagttc ctcactaact ctgtgtggcc ttgggcaagg ttgggcctgt 5640

gttaacagat tatgaccctg ggctctcaag ctagaggatc taaatttgaa tcctggctct 5700

gctaaagcaa ttagtgatgt aaactttaat gggtcagtta accttcctgt ggcttagttt 5760

gctcatctgt aaaataggga tcataacagt atcaatacca catgattgtt ggacagattg 5820

aatcagttaa tgcaggggaa gtacttagca tgacacgtat tcactatcat ttcctggagt 5880

aagagctgtg tgtgagtggg tgtgagcatg tgtgaaacct tttctctgca atctcagtta 5940

agaaaccaat ccagaattta aagttcaggg cctaaatggg tggttatctt ctcccagttc 6000

catcctatcc caccttttgct cttcctcccg cccacaggag ctgttggtcc ttgattgggc 6060

tggaagacct ggtggaccct aagtgatcta taagaggaga atagagaaca gggaatgtct 6120

tcaaaaatct agagggacac agaggctgag aggcaggcag tcctgcaggg tcttctgatt 6180
gggacaagga gaaccttggt cttcacaggc caattctggt cagtttcccc catggacaga 6240
tgaggaaaca ggcccaggaa tatccaaggt ctcacacttc ccatctgtca agtcttgttg 6300
attctgttgt attcatgtct ctcaaaggga gatagagttt agggaagaaa gaaggatcaa 6360
ctgtgtctga taccactggg agcttaagta aagggttctt ttacttcata gcatttatcc 6420
caatttgtaa ttcagtatta tttgtgtggc tgtttggtgt ctctttctcc tatatgagtg 6480
ctagcttcat aagggcaagg attttgattc tttaatattt agtgcttgcc acatgccctg 6540
aacacagcag gcatacaggc taaccaacat acagtggcat gaaagtcatg aaagtgagac 6600
acctacctcc tccagtgcca agagagcata accatgcacc tgtcactctc ctcaacacca 6660
cccccaagca tgaggcccaa aagcattagc taatcccctc ctccagccac taaaacttaa 6720
aggccaggtg tggtggctcc catctgaaat cccagaactt caggagacag cagcaggagg 6780
atcacttgag gccaggagtt tgagatcagc ctgggcaaca tagctaggtc ccatctgtac 6840
taaaaattag ctgggcgttg ttgcatgcct gtagtcccag ctactaagga ggctgaggtg 6900
ggaggatcac ttgagcccag gaggtggaaa caacagtaag ctataatcac agcactgaac 6960
tctagcctgg gcaacagagt gacaccctgc ctcaaaacaa ttttaaaaat aaataagagc 7020
aaaacttaga taccacgtgg tcaccccaac atgcaaaatc aagttttccc ctactgagaa 7080
gaatggggac ttgacagctg agttacagag agataatctt cttcttcttt ttttttttt 7140
ggtttacatc ctcaagatca tgacttgtga aatttgaatc gaatacacat gtaattccag 7200
agcaatgttg cctccgcata ccatcagcaa ttcacttggc tactggaagt caggataagc 7260
ttcccagaag agaggtacca cttgggctac caatataaaa ggatgaaaat atcagagtga 7320
tggtgttctt tacaacgttg agtccctgga cagcctgtcc actgatgctg atatctgagc 7380
ctaatgcttc tctgaatgtt gagattgaac tttgatccaa tgaaactaga acgagaaaga 7440
agataagtct ttcattgttg ataaggacat tatgtttctc atacttgtat gattattttt 7500
ccttagctgt actataatta tctgcttatt tgtctctgct ctatgtgctt agggtacaaa 7560
gttgaccaag accaactttg gttggaagca tagtactaag agcacagtac tgagagcaca 7620
gtattgagag cacagcttta aaaaacatga tgaaggcttt aatacaggaa atgagcaggg 7680
gagaggcatg tggtggttgg atgtatcttc cttgacacag tcagtgcagc tctcagtagt 7740
caagtcccta catgttagaa gatgttacct tctgtggaat taagtggcag aacttgcctt 7800
caattatttt cctttgcaga acaacaccaa ctgcattagt taggacacag tgctggctgc 7860
atttaagtcc caagcgatga ttagtctctc actgttggta tagattcaaa ccaatcagac 7920
cacctcctaa agtttgtagg gcaggtaaat cctcatctta gaataaaaat catcttacca 7980
agtatgtgtt ttagaggcaa gaagaaaaca tatttgtttc tgtaagagtt ttgtttaaaa 8040

aaaatataag aaaggctctc ggtttaggtg aggtaatgaa gttgttgata gttatcagat 8100

gacactggaa tctttacttc tctgaacgtg ttctgtgcat ctctcagtgt gggaacatag 8160

agagggagat cctccagcaa tgccactgat atggtcagaa actgcatctt tctttctccc 8220

tgctgagatg agatggagtc ctttgttcta gaagacccat ggtggtgccg ctgggagtaa 8280

cccttgagac aggaacacaa atcccaacca atttgtggtt gcagccttga gtctcactat 8340

ttcccatagt gatgcgtagc agggaatggc aggtgcacca gagcaggaga ggacctaata 8400

tctcccttcc tgttagcttt ttataaagtt ttattgtgat cagtagcagt tgggaagcta 8460

cttgcagtca ctgagcctca gtttctacat ctgtaaactg gggatagtag catggcccct 8520

acttaatgtg ctcagcaaag ccactgaaag gagacagaaa tgtatctaaa ttaccctgga 8580

cttttatcct acctctcttg gggattgtca ccaccttccc atgtttgtcc tttttggttt 8640

gatgcttgct gtcacttctt tccttaggtg cctctctgta cggctctttt atcccaggga 8700

ttccagagtt acagcacatg cataccacca tccaagcatg tttatttgtc tcctgcttca 8760

ctaggctgtc cccaaggaac atgtggctcc cggcacacac ctggcacaac actgcacatg 8820

acattcaccc acttggcctt gaatctgaca aggaatctgg catgatgttc acccactcag 8880

gccaggtgcc gagcagccct ggaggcttag gggccagagg gatgggaaaa ggtgtctttc 8940

tggggtgagt atcagtttct gcaggagggc tgaatgtgag aaagaataaa gagagaagga 9000

agcgaacaag cacagcttaa acatcgccta tttctattga gttttaagaa cgctgtgatt 9060

ttgtttgtca tgcaatccat tcatcaggcc aggcagacac agaacttggg tgtgagtgac 9120

gataatgagc tgatataatt ttcacaccct catcactgag atctctccca tcaggaatgg 9180

gtcagggagc tcacaggtgg cagcaactgc tattacaggc ctcatctcta ccagctcctg 9240

gggcctgccc tcctcccatt agaaaatcct ccacttgtca aaaaggaagc catttgcttt 9300

gaactccaat tccaccccca agaggctggg accatcttac tggagtcctt gatgctgtgt 9360

gacctgcagt gaccactgcc ccatcattgc tggctgaggt ggttggggtc catctggcta 9420

tctgggcagc tgttctcttc tctcctttct ctcctgtttc cagacatgca gtatttccag 9480

agagaagggg ccactctttg gcaaagaacc tgtctaactt gctatctatg gcaggacctt 9540

tgaagggttc acaggaagca gcacaaattg atactattcc accaagccat cagctccatc 9600

tcatccatgc cctgtctctc ctttaggggt ccccttgcca acagaatcac agaggaccag 9660

cctgaaagtg cagagacagc agctgaggca cagccaagag ctctggctgt attaatgacc 9720

taagaagtca ccagaaagtc agaagggatg acatgcagag gcccagcaat ctcagctaag 9780

tcaactccac cagcctttct agttgcccac tgtgtgtaca gcaccctggt agggaccaga 9840

gccatgacag ggaataagac tagactatgc ccttgaggag ctcacctctg ttcagggaaa 9900

caggcgtgga aacacaatgg tggtaaagag gaaagaggac aataggattg catgaagggg 9960

atggaaggtg cccaggggag gaaatggtta catctgtgtg aggagtttgg tgaggaaaga 10020
ctctaagaga aggctctgtc tgtctgggtt tggaaggatg tgtaggagtc ttctaggggg 10080
cacaggcaca ctccaggcat aggtaaagat ctgtaggtgt ggcttgttgg gatgaatttc 10140
aagtattttg gaatgaggac agccatagag acaagggcaa gagagaggcg atttaataga 10200
ttttatgcca atggctccac ttgagtttct gataagaacc cagaaccctt ggactcccca 10260
gtaacattga ttgagttgtt tatgatacct catagaatat gaactcaaag gaggtcagtg 10320
agtggtgtgt gtgtgattct ttgccaactt ccaaggtgga gaagcctctt ccaactgcag 10380
gcagagcaca ggtggccctg ctactggctg cagctccagc cctgcctcct tctctagcat 10440
ataaacaatc caacagcctc actgaatcac tgctgtgcag ggcaggaaag ctccatgcac 10500
atagcccagc aaagagcaac acagagctga aaggaagact cagaggagag agataagtaa 10560
ggaaagtagt gatggctctc atcccagact tggccatgga aacctggctt ctcctggctg 10620
tcagcctggt gctcctctat ctgtgagtaa ctgtccaggc tcctcttctc tgtttccttg 10680
gacttggggc gctaatcacg cctctctttc ccttatctgg attgaagatc aaaaaagatg 10740
ttcaggccgg gcgtggtggc ttacacctgt aatcccagca ctttgggagg ctaaggcaag 10800
tggactgcct gaggtcaaga gtccaagacc agcctggcta acatggcgat actctgtctc 10860
tactaaaaat acaaaaatta gctgggcatg gtggtgcacg cctgtattcc cagttacttg 10920
ggaggctgag gcaggagaat tgcttgaacc cggcaggcgg aggttgcagt gagctgagat 10980
catgccagtg cacttcagcc tgggtgacag agtgaggctg tcttaaaaaa aaaaaaaaaa 11040
aaaaaaagat gttcaaggag cagtagctta agtgttggat gctacaaaca tatagaggtt 11100
attgtagatc ttatgcagct ctataaagga ataaataagc atcttcccca tccatcttta 11160
gtggcaagaa gggttttggg atagcattga ttgaggatga tctacttgac aatagtttgg 11220
acccaaggag gataaggaag gaaagtagtg acggatctca ttccaaactt ggctgtggaa 11280
acctggcttc tccttactaa actagaattt ggattttaca ttttcccctt tatgttgcag 11340
tagaagagga tgaatcctct cactggtggg atcctgccat cctagagcag gtagagagaa 11400
gagtcactcc ccactgtggg tagtggaggc ttctcacatg tcacatttca cttctacctc 11460
aatttcactc ttactaagat ttgggaatca taatgacagg aaaatagaaa atataaacct 11520
cattttaatt ctttcacaga aaggttagaa attcagtgag ttgtggcaac atattttcca 11580
tcttctgacc ttttaacact aattgatatg gcttaaattc attctatttt aaaccagatt 11640
tttttggaga tagtctattt ccaacatgtt ccttctaggt gacaaatgag ggctgttagt 11700
tcagtatttg ttacaataaa tgtgtgtaaa ataacctcac ctttccagaa tcatgtcagg 11760
aatatgaatc taatgcacaa atgtataact ctatgacaag attgcatata tcttttaaaa 11820
tataccttcc caacgttcat tttaataccc ctatttcaaa caaacctgct tagcaggtta 11880

tgttaaacgc tcagggcaga ggagtaagca agactgtgag ccagtgatga cagcaaaagc 11940

atccaggtag gatcaaaatg gagtaagaaa atattcctca tccctcaggg tagaactcca 12000

aagagatatt catgggtcct ggccccgtag tggaggtcac tcaaaggaca aacatgtttg 12060

catctcatct gcttgaagcc tggacacaga ggcaccatct gtgtcactct gtgtgtggtc 12120

tgccatgttg tggggtggtc actacagact cacagactag gcagctgggc agacaatacc 12180

ttagccttag atgatgctga tgcagcccag gagtcagaaa ctgtagtgca gacaatgccc 12240

tccttaggcc aacacaatta agtgcaatag atgactggct tttctgttag cctcttcatt 12300

ggaaccaaaa gcagcattac tctaccaaac agaggggagc tggaaagaaa ctacacagtt 12360

tgcccagcct agcctctgcc ttgacacgga accatgtgag tctagacatt cacctagatc 12420

attccttggg gaccaatgct actgacacat taactcaata gtttgtcctg gcctgagagg 12480

tcatgtaact tgtagaaagt ttagaagcag agattagtgt catttatttg ccatggctgt 12540

gacaacaaag gaaggaacag gagtgggaaa acccaaggcc accctggttt tggtagatgg 12600

tgcacacgct tccactagct gttctggggc aaagatccaa atgcactatt gggcctggct 12660

atgctgcttc tgctgggtcc cccaaacatg agcctccacg ccatttctca gttgtatttt 12720

accacatatt atcacagtca ccggatttgt acagaatatt tggaacctat actgtcttaa 12780

gggctaccct ttaaagaaga gaaaacaagg ttttaattca actgtctgga acattttatg 12840

tttacttatg tggaatacta catcttttgt tataaacagg agggaatgtg gacattcgaa 12900

ggcccctacc ttttagctaa aagcccatat gaagcatatg gatccattta tacacaccat 12960

gcttttcagc tacattttcc taatttgcct ctctggggcc aaccttgtgg gactagcaga 13020

ttcatggttg agttgaagga tggtgacctc ttccatcagc ttttcttctt cctccagtct 13080

tccaaccctc agtaacatca gactgggaag gtcttcagac atccagaaac cccagttcgg 13140

ggagttcata catgacccat caaagatgag ttgcaagcag gcctgcctta gggagcacca 13200

gccttaatgg gttttcctac agagatagtt gatgggcaga tgcaataaac tgactgcttt 13260

gtgattgacc accttgagaa aaatagcatg tctggctatg ttagtctttt cttgcattgt 13320

tataaagaaa taccagagtc tgggtattta taaagaaaag ggatttaatt gtctcatggt 13380

tctgcaggct gtacagaaag catagtgact tcttcctcta gggaggtctc gggaaattta 13440

caatcatggc agaaggtgaa ggagaagcag acagatctta catggctgga gcagaagcaa 13500

gagaggctgg ggagaaggcg ccacacattc aaaccaccag atctcataaa aactcattgt 13560

cacgaggaca acacctaagg cgggatggtg tgaaacgatg agaaactgcc cctaggatcc 13620

aatcatctcc taccaggccc cacctccagt attggggatt gcatttcaac atgagatttt 13680

ggtaggggca cagattcaga ccatatcact ggcactgtgc taatcagatg aatatcacca 13740

gttggaaggc tagattccac aagaggagga atgacctgga aattggttct ttagttgtga 13800

ttcttctgca cactgtcatt cagggaaata tgagtcaatc atccttccca ataggtcaaa 13860

tcaaccagat catctgatca tagagactga ggtgtagctg aaagctgctc acatttctat 13920

gaggtcaatg gaagccttga gcacagttgt caatctgtag aaataaggac tctgtgactc 13980

ctccaagacc tctctgtgaa tgacggttta agaagaacca gatcctaaaa cagggtcaga 14040

gcttagaggg aagggaaagc ataaaagcct ctgagcaaat tctaaagaca gggtcaccat 14100

aggctctcag tgaccctctg tgactgagtg gctgcagtga tgcaaaatct catcatcact 14160

gcggaagaca aaaaaatgtc acccтttcta cctaggatga gaatccccaa atttggggag 14220

aggccactta ctaaatagac gtaaaggaac aaagtgacct ggaagaattc ctgcctgaac 14280

ctctcaggat cattcacatt tgagaacatt tatcaaatat tcattccagg actgggacca 14340

tgaagacttc agctgctttg agctaatcat tgtaactttt tggtgtctca tggtggaggc 14400

aggaaaggac ctgatgaaca aatataatca ttgccgtcag agttactgtt attatttctt 14460

gccttaatgt tacctcgttc tcttgagcat tccagttcct cagtcaatga ctcatcaacc 14520

cctatatcta taaagtcaca atcgctgtga cttgatttct gtttcacttt gtagatatgg 14580

aacccattca catggacttt ttaagaagct tggaattcca gggcccacac ctctgccttt 14640

tttgggaaat attttgtcct accataaggt gagtgttttt gagctcactc ttttgcttct 14700

tatgattgcc aagagcagct tagttccatc agtaaaaatg cttctcctca gggggaaggt 14760

ctgaagtttt acactttcag aaacagtgtg taggcatcac ccagaacatg gcaatgttta 14820

cccaagggct ctcttgctaa ctctcaggaa cctcaggttt gcctcagttg aacagcccaa 14880

atctcaggta gatcagcaac ctgatgctca gaacttgatg tgcaaacttt gtgagcgcgc 14940

cataaagaag gttttctttt tgctctatgc aggttcccag gaaggtacag tcatacttag 15000

ttagtattaa aagtaggaaa aggacccccт gattgtgact tgttatctgt gtacatgaga 15060

gtcaaacttt cctctctgta gcaagagctc ttgagtagcc ttttttccct tccttctgga 15120

cagctttgaa actcaattta ttagggagcc caggtattta cctttgggtc atttgcacct 15180

gcttcaatcc tctccgaaaa atgctaaatt ccctgagggt atctccatgg ctctacccca 15240

gctcttactc cccatgacat cttttgcagc tttgagagac agaacaaagg ggttctgctt 15300

tatttctttt ccttcaaagg ctgcacctta tgggtgagac tgatcacaga ctggatataa 15360

ctgagatgag acagtggtgg tcaatcaaac tcagatattt aagcacaaaa tgagtttgtg 15420

gggtttttтt ttacacaaag gcggaatcac atgcaaaatc actagaaagg ggatgatttg 15480

atgaaattat taaatattta attttgctga atagaatata atatgtgcca cgtggaccgt 15540

gaactttggc cgagcctttg tgcctaacct agtctgatgc tctgcccagg gtctgggccc 15600

tggatggaaa attaggagcc catgtccaca tggccagccg cagcagtcag ctctttggct 15660

tacatcatct ttcccacata cctgaggctt gtttctcaga ttctaattct ctcaggtgag 15720

ggctttgttg tctaattact atccaggaat ttcatatttt ttccctgtgc aaaagcaata 15780

atttccccgc cacctttttcc aggtcaactc tttagtagat gtacccccaa gatgcacatt 15840

cctgggacct ttgtttgcac agttaaaatg tcacccctga aatgtcgata caggaaggtt 15900

tgtttttaag tttcagtgaa aactctgagc aagtgttgta atttgctgtg tccgatgtgt 15960

agaggggaca ttttctcaga acttccatgt taagctggaa aactggaaag tgagttcact 16020

ttgtcattct gtcactcgtt cattttctca ctcaacaaca tgcctcatac ttacctaaat 16080

ctgctagact aaaggagttc cctggtgtct gtactttcca attctgctag aactctagag 16140

cgagctcatg aaataaatga aaaggatgac aaagagataa aacactgtgc attctcttct 16200

gatgctaatt cactttccct tggcctcagt ttccccatgt gcccctggag gtgatcattc 16260

agggattcat gagattttca agacaacaca tgaaaaagca aaaagacatc agaaagacaa 16320

agaggtactt agtatttata cacaaggata agtcattcag tatccacaac acttggagag 16380

aattcaagag tgattttaaa tttccctttt caaatacctc ctctgttttc tcttatttcc 16440

tttatgacgt ctccaaataa gcttcctcta actgccagca agtctgattt cattggcttc 16500

gactgttttc atcccaatta gaggcagggt taagtacatt aaaaatataa atcaaatatt 16560

attttgtttc tcctcccagg gcttttgtat gtttgacatg gaatgtcata aaaagtatgg 16620

aaaagtgtgg gggtgagtat tctggaaact tccattggat agacttgttt ctatgatgag 16680

tttaccccac tgcacagagg acagtctcag cccaaagcct cttgggatga agctcttgtc 16740

aacctaacta caaacagaga gaagttctct gaaagaagaa gatatttatt tgggtgtaga 16800

gtattgcaat gggaatctgc atgcctttat aaactatgtg caaattcagg gaagtaaagc 16860

aagacaaaga ggctccaagg aaaatatgag gaggatttct tatcagtttt gaaataatta 16920

tccttcgcta caaagatcag taacaagggt gacgcctcac caaggttgga caggcagttg 16980

ctgggcaggt gtccttgcag aaatattttt tttaatgttg ggatggcctt tgtgcaagct 17040

tgtagttttg cggagtcttt tgtgatagtt ttgttatcag gcacacaagc atgagaatcc 17100

tctcttcata gccttctttg atttatttgt cagggttttt acacacacac acacacacac 17160

acacacacac acaactagtg acatcatttt ggttctaaca acattcacac tggttattgt 17220

aaaacttttc gaaggttgtc ctaccaagga tcccatgtgt caccaggtgt caagttctac 17280

agtctgaact aggctgggag cattgtgatt acttttctcc agactttggt ggcccaggga 17340

ctcacagcat catgctctgt ccagtgtctg cctattcccc tcttcttttt ttttttcctt 17400

aggtgccctt ttattacatg tgttgtctca gacccttcta atatgtgctc ataaatacat 17460

catatcatct ccttcccaca tcaattcact ttcaattaaa agccaaaact ctttcattta 17520

gactttggat ttaaagtgct tttgaatgaa gggttgagag ataatagaga aatagattgg 17580

caaaccattt atactctgct gttgttgttt tttaatttta tctgcaagtg tggaactttt 17640

cattctgttt tgttattaaa tttaagccaa gacttttttaa tagaagggta tataagcatt 17700
tctttgtcta taccttcctg ctgaatttga agaaatgctg aatattctta accactggcg 17760
ggctgatgga ctgtgatttt attttatttt ttatttttag ttttttaaat tataccttaa 17820
gttctgggtt acatgcatag aatgtgtagt tttgttacat aggtatacac gtgccatggt 17880
ggtttgctgc acccatcaac ctgtcaccta cattaggtat ttctcctaat gctatctctc 17940
ccctagcccc ccacccaaca acaggcccca gtgtgtgatg tttccctccc cgtgtccatg 18000
tgttctcatt gttcaactcc tacttaggag tgagaacatg tggtgttgag ttttctgatc 18060
ttgtgatagt ttgctgagaa tgatggtttc cagcttcatc cttgtccctg caaaggacat 18120
gaactcattg ttttttttatg gctgcatagt attccatggg gtatacgtgg cacattttct 18180
ttatccagtc tgtcactgat ggacatttgg gttggttcca agtctttggt attgtgaata 18240
gttctgcaat aaacatatgc gtgcatgtgt ctttatcata gaatgattta tgctttgggt 18300
atatgcccag taatgggatt gctgggtcaa atggtatttc tagttctaga tccttgagga 18360
atcaccacac tgtcttccac aatggttgaa ctaatttaca ctcccaccaa cagtgtaaaa 18420
gtgttcctat ttctccacat cctctccagc atctgttgtt tcctgacttt ttaatgatca 18480
ccataccacc tggcatgaga tggtatctca ttgtggtttt gatttgcatt tctctaatga 18540
ccagtgatga tgagcatttt ttcacatgtc tgttggctgc atagatgtct tcttttgaga 18600
agtgtctgtt catatccttt gcctattttt tgatggggtt gtttgctttt tttcttgtaa 18660
atttgtttaa gttctttgta gattctggat gttagccctt cgtcagatgg atagattgca 18720
aaaatttttct cccattctgt aggttgcctg tttgctctga tgatagtttc ttttgctgtg 18780
tagaagctct ttagtttaat catatcccat ttgtcaattt tggcttttgt tgccattgct 18840
tttggtgtta tatttatgaa gcctttgccc atgcctgtgt cctgaatggt attgcccagg 18900
ttttcttcta ggatttttat ggtcctaggt cttacattta agtctttaat ccatcttgag 18960
ttaatttttg tataaggtgt aaggaagggg tccagtttca attttctgca tatggctagg 19020
cagtttcacc aacaccattt attaaatagg aaatcttttc cccattgctt ttgtgtgtca 19080
ggtttgtcaa acatcagatg gtagtagatg catggtgtta tttctgaggc ctctgttctg 19140
ttccattgat ctatatttct gttttggtac ctgtaccatg ctgttttggt tactgtagcc 19200
ttttagtata atttgaagtc aggtagcgtg atgcctccag ttttgttctt tttgcttagg 19260
attgtcttgt ctatgtgggc tctttttttgg ttccatatga actttaaagt agtttttttcc 19320
aattctatga ggaaagtcag tggtagcttg atggaaatag cattgaatct ataaattacc 19380
ttgggcagta tggccatttt catgatatgg agtcttccta cccatgagca tggaatgttc 19440
ttccatttgt ttgtgtcctc ttttatttca ttgagcagcg gtttgtagtt ctccttgaag 19500
aggagaactt cacatccctt gtaagctgga ttcctagata ttttattctc tttgtagtaa 19560

ttgtgaatgg gagttcactc atgatttggc tctctgtttg tctattattg gtgtgtagga 19620

atgcttgtga tttttgtaaa ttgattttgt atcctgaggc tttcctgaag ttgcttatca 19680

gcttaaggag ttttggggct gagacgatgg ggttttctaa atatacaatc atgtcatctg 19740

caaacagaga caatttgact tcctcttttc ctaattgaat atccatttct ttctcttgcc 19800

tgattgccct attcagaact tccgacacta tgttgaatag gagtggtgag agaggacatc 19860

cttgtcttgt gccggttttc aaagggaatg cttctagttt ttgcccattc agtatgatat 19920

tggctgtagg tttgtcataa atagctctta ctattttgag atacgttcca ttgataccta 19980

gtttattcag agtttttagc atgaaaggct gttgaatttt gtcaaaggcc ttttctgcat 20040

ctattgaggt aattatgtgg tttttgtcat tggttctgtt tatgtgatgg attacattta 20100

ttgatttggt attttgaacc cagccttgca tcccagggat gatgctgact tgatcctggt 20160

ggataagttt tttgatgttt tgctggattt gatttgccag tattttattg aggattttcg 20220

catcgatatt cattagggat attggactaa aattctcttt ttttgttgtg tctctgtcag 20280

gctttggtat caggagatac tggcctcata aaatgagtta gggaggattc cctccttttc 20340

tattgttcag aaaaatttca gaaggaatga taacagctcc tctttgtatc tctggtagaa 20400

ttcagctgtg aatccatttg gtcctggact ttttttggtt ggtagcctat taataattgc 20460

ctcaattcaa aacctattat tggtctattc agagattcaa cttcttcctg gtttagtctt 20520

gggaggggggc atgtgtccag gaatttatct atttcttcta gattttctag tttatttgca 20580

tagaggtgtt tatagtattc tctgatggta atttgcattt ctgtgggatc agtggtgata 20640

tccttttttat cattatttat cgcatctatt tgattctgct tttttcttta ttagtcttgc 20700

tagcagtcta tcatattttg ttgacctttt tcaaaaaacc agctcctggc ttctctcatt 20760

ttttgaaggg tttgttgtgt ctcaatctcc ttctgttctg ctctgatctt agggctcagt 20820

caacgtagca tagccacagt aactcccgcc tctcgatggt aaggggaacg ttacagagtc 20880

aggaatcgac ctatcctgca ttctctgggg ggcaatatct tagttatttc ttgtcttctg 20940

ctagcttttg aatttgttta ctcttgcttc tctagttctg ttaattgtga tgttactgtg 21000

tcaattttag atctttcctg ctttctctag tgggcattta atgctataaa tttccctcta 21060

cacactgctt taaatgtgtc ccagagattc tggtacattg tgcctttgtt ctcattggtt 21120

tcatagaaca tctttatttc tgccttcact tccttattta cccggtagtc attcaggagc 21180

aagttgttca gtttccatgt agttgtgtga ttttgagtca ctttcttaat catgagttgt 21240

aatttgattt cactgtggtc tgagagacag tttgttgtga tttcttttct tttacatttg 21300

ctgaggagta tattacttcc aattatgtgg tcaattttag aataagtgcg atgtggtgct 21360

gagaagaatg tatattctgt taatttgggg tggagatttc tgtagatgtc tattaggtcc 21420

tcttggtcca gagctgagtt caagttctga atatccttgt taattttctg tcttgttgat 21480

ctgtctaata ttgacagtgg ggtgttaaaa tctcccatta ttattgtgtg gaaatcttag 21540
tctctttgta ggtctctaag aacttgcttt atgaatctgg gtgctcctgt atttgggtgc 21600
atatatattt aggatattta gctcttcctg ttgaattgat cccatcacca ttatgtaatg 21660
cccatctttg tctcttttga tctttgttgg tttaatattc tttttaaaat aaaatatttt 21720
aaacatatga aacattatgg agaatggcat gggaaatatc cacgtatgca ccacccagct 21780
taacaaatgc tctactgtca tttctaacca tggtctcttt gaagagctct tttgtctttc 21840
aatgtctctt ccttgtttgg cccacattat ccttcatcat atgaagactt gggtggctcc 21900
tgtgtcagac tcttgctgtg tgtcatacct aatgaactag aacctaagat tactgtgtat 21960
tgtacaacta agggattatg taaagtcagg atcaaagtct ggcttcctgg gttgggctcc 22020
agctgtagaa taaggctgtt gatgtttaat caactctgtt tttttcacac agcttttatg 22080
atggtcaaca gcctgtgctg gctatcacag atcctgacat gatcaaaaca gtgctagtga 22140
aagaatgtta ttctgtcttc acaaaccgga gggtaagcat tcatgtgttg aaattaaaat 22200
actgattgat taaatttata ttttgaaatt cttatatatt catagacagt tgoctaaaaa 22260
atgtccagga aggttccacg tccacttcat cctgtccccc ccgaatggta acatcttgca 22320
atcttgcata actataaata cagtatattc atgttactat atagtacagg aaattgacat 22380
tgatacagtt cacagagctt attcagattt caccagcttt atgtgccctc atttctgttc 22440
tatgcaaatt tatcacaatc atagatttgt gcaatgacca gcatgatcaa aacgcagaac 22500
ccatttgtgt tctatacaaa tttatcacat cattagtaga tttgtgcaat gaccagcatg 22560
atcaagatgc agatccactc tgtctccatg tggctccctc ctgctatcct acagtcacaa 22620
gtctttttct ctgacagggt ccatatcaga gcaaactatt ttttattttg aggtgatcaa 22680
tgtattaata tttccttttc tggattgtac ttttggtgcc atgtttgaaa gttctttgcc 22740
tagccctcct tcctatattg ctgtttttt ctaaaagtca taaagtttaa cgctttacta 22800
aatgtagctc tataatcaat tttgtgttat tttttgtata aggtctgaga tttagatcaa 22860
ggttcatttt ttttgtggct tatggctgtc caattcctcc aacgccattt ttggaaagat 22920
gggtatattg ttaaaaatca actgggcata cttctttgca tctctcacgt actactgtgt 22980
cccattgatc actgtgttta ttattccacc aataccacac tgtgttgacc ctagtagctg 23040
tacactaact cttaacctcg tgtagagtga ttcttcccac ttttattgac ttatttttc 23100
agatttgttt taactcttcc tggtcctctg cttttccata aaaattcaga atgagtttct 23160
cagtgtctac aaataaacgt gctgttattt tgacaagaat tgaattaaat atatagacca 23220
gtttatggaa aatgtgtatc tttactgttt gatctttcaa ttcatgaaca tagtatgcct 23280
ctccatttcc ttagattttc tttgattgct tttaacatct tgtagttttc agcatagaga 23340
tcctgtacat gttttgttag atttacagct aaactatttc atttttgttg gaatgaccgt 23400

aaatgatatt atgtttttct tgtattttca gatattgatt gttgttacat agaaatgtgc 23460

tttgattttg tgtgttgatc tggtatccta gaaccttgca gaactgacat agtagttcta 23520

gaagtctctt tgtatatgcc ttgagatttt acacattgtc agttatgtca cttgaaaata 23580

gagacaattc ttttatttcc tttccaatct gtatgccttt tatttctttt cttttgtcta 23640

ttgcactagg acttcccagt ataatgttga gtaaatgtgg tgaatttttg aattgttcct 23700

aatcttagga gggaagcctt cagttctttc atcattaagc atcatttaga cgaagtgggc 23760

tgtttttttg tagattctct ttatcaaatt gaggaatttt ctctccctag tttgctgagt 23820

ttttatcata aatgaatgct ggaagtactc attataaaaa aaatggctat ggaagatgaa 23880

agaaagtttc aagcatgttg gcttgatagg ccagttccaa gttggcaaaa ataattatct 23940

ctttttttctt tctatccatg aaataaaaaa ttaagagcca agaatgttta tggaattgca 24000

ttatttcttc aaaatatgtt cctagtttta aaggtattac ctactatttc ttttaaaacc 24060

atcacattga ggcacttctt tttcacgttg cccatgctgc aggagaacat aaagacagct 24120

tgtctgaggc aacatacaat ccaccaaagt cacctgcttg tctgtctcca ctccgtctct 24180

acactgcaga agtgctaggt cttgattctg tttattgtac tggaagaaca cattctctac 24240

cacgtggata atttgcatgt aaaagaagac tgggatatag aggctggaga cgacatcagg 24300

gtctcctgaa cactgccgcc acccccccgc cccgccccac acaaatacat cccaggacac 24360

tgggcatctg ggataaatct ctattgagca tctagcatag ggcccatcac ccagtagaca 24420

gtcactaaat agttgttgaa taagtgttcc tgtttaacac attttctaca accatggaga 24480

cctccacaac tgatgtagga caaaatgttt ctgctttgaa ctctagcctt ttggtccagt 24540

gggatttatg aaaagtgcca tctctatagc tgaggatgaa gaatggaaga gattacgatc 24600

attgctgtct ccaaccttca ccagtggaaa actcaaggag gtatgaaaat aacatgagtt 24660

ttaataagaa acttaaagaa tgaatctggt ggggacaggt ataaaataag atcacagtcc 24720

ctttccaagg ggtagtccac tgaatttgag ctgcctaaaa atggtctttt atctttatgt 24780

acagaaaaca catcacaaaa ttcattataa aatgtcactt actgctccat gctggggaaa 24840

gccatgtcct tctgggacta gagtctgcac atttaactat gggtggtgtt gtgttttgtg 24900

cttagatggt ccctatcatt gcccagtatg gagatgtgtt ggtgagaaat ctgaggcggg 24960

aagcagagac aggcaagcct gtcaccttga aagagtaagt agaagcgcag ccatggggtt 25020

ctgagctgtc atgaacccct ccagctgcct gccatggagc tgatattcct gctgttgggt 25080

tattccagtg accagacaaa aggagggctg tggtaatgca acttcaatgg gtctcccaag 25140

atggggcagc tccgatgagg aggtggggca gctggaggaa aaggatcttc tcccctgtgc 25200

acaggggcca gggtttacat atccattaaa ttgtcacctt ggatattcta gaagactaaa 25260

tatatccttt agggggaaaa agtgtgattg taccaaagtt ttaagcatgg agtgtatggg 25320

atggtggaag gggaaggcac ttggtatctg ttggttggca gtgagtaggt tgggagagtt 25380
ataatggaga acttagaata actttgatca tttcatgttt ttttctgagg atatcagtag 25440
aatactaaat attaaaattc ctaccatttc tttttcctcc agtctcaaag agagagggtg 25500
gtaaaaacac tataggtagg gcaagcctat tatttgctat ctacacttat gcagtaaaaa 25560
caggtgtaat ctgagtttgt cctgggcaga ccagggatat gtggtcactc actatagaaa 25620
tttccaaatc aaattttgag agatttttt ttaaccagga cattattggt cattatattt 25680
tacaaaaata attctgctgt cagggcaacc tcagctcacc acagctgggg atagtggaat 25740
tttccaaagc ttgagcaggg agtatagaga ataaggatga tatttctagg agctcagaac 25800
agggtactgt tgctttgtaa agtgctgaag aggaatcggc tctgggcata gagtctgcag 25860
tcaggcaata tcacctgtct tgagcccctt aggaagagtt aattattcta ctcttgttct 25920
gctgaagcac agtgcttacc catcttgtat catccacaat caatacatgc tactgtagtt 25980
gtctgatagt gggtctctgt cttcctatga tgggctcctt gatctcagag gtaggtctaa 26040
ttcagttcag tgtctccatc acacccagcg tagggccagc tgcatcactg gcacctgata 26100
acaccttctg atggagtgtg atagaaggtg atctagtaga tctgaaagtc tgtggctgtt 26160
tgtctgtctt gactggacat gtgggtttcc tgttgcatgc atagaggaag gatggtaaaa 26220
aggtgctgat tttaattttc cacatctttc tccactcagc gtctttgggg cctacagcat 26280
ggatgtgatc actagcacat catttggagt gaacatcgac tctctcaaca atccacaaga 26340
ccccttttgtg gaaaacacca agaagctttt aagatttgat tttttggatc cattctttct 26400
ctcaataagt atgtggacta ctatttcctt taatttatct ttctctctta aaaataactg 26460
ctttattgag atataaatca ccatgtaatt catccactta aaatatacag ttcagtgatt 26520
tgtagtacat ttgaagatat gtgtgaccat catcatttta aactttaaaa ctttttttgt 26580
caatctagag acctcataca tttttagcta tcagcccccc gtcacaaacc ctgtcatcat 26640
atgcaaccac taatcaactt tctgcttcta tggatttgcc tattctggac acttcataga 26700
aatgatatta attcatcagg gtttttttatt ctctagttca tgaatttgta ctttagtctg 26760
tatcattttc tttcttctgc tggcttcagg cttagtttgc ccttcttcgt ttactatgtt 26820
gtggcatgaa catagattac tgatttgtga tttttttgtt cctctaaatt tagacattac 26880
agctgtaact ttccctctga gcacttcctt tgctaaatcc catgagattg tggcctatca 26940
catcttagtt ttgttcacct caaaacagtt tctatttgcc ctttgggttt ctactttgac 27000
tcattgggta cttaaatgtt tattatttaa cttccacata tgtgtgagtt tctcaatttt 27060
ctttcccttа ttgattttat ctttattcca tgataggtga cagagatatg ctgtgttatt 27120
tctatcttga ctacctacta tttcttgaac agcaagatta attttgagct tcagattatg 27180
atttgggtta ttctaggaga ctgtagtcca atagataaag gcaaagagat tagggcattg 27240

aattttgttc cttttatcct tcaaaagatg cacaaggggc tgctgatctc actgctgtag 27300

cggtgctcct tatgcataga cctgcccttg ctcagccact ggcctgaaag aggggcaaaa 27360

gtcatagaag gaatggcttc cagttgagaa ccttgatgtc ttttactctt ctggttggta 27420

gagaaaacta gaattgctcc aggtaaattt tgcacattca caatgaattt ctttttctgt 27480

ttttgttttg tttttcctac agcagtcttt ccattcctca tcccaattct tgaagtatta 27540

aatatctgtg tgtttccaag agaagttaca aatttttaa gaaaatctgt aaaaaggatg 27600

aaagaaagtc gcctcgaaga tacacaaaag gtaaaatgtg gtggtagtta taggaggatg 27660

tttagttttt cataattttt tagataatat acatatgatc agtgcagtta cctgtatgtt 27720

tttaaagaat gcttttaaca tgaagactgc tcatgtttag agcaagagaa ttcatttggt 27780

agaaatgcag aaagtggggt ttggggaagg agatatgaga atgagtcaga gacagcacat 27840

gaaatttgat atcagacaca acaattagta tgccacggca taaattttat tgagataaaa 27900

ctttaccact ttacttccct tcaataaatt gtcagaggat aaacattact gtttggaaat 27960

atattttact gatattatgc tttccccaga tcataaattg gtaaagactc atttcaagta 28020

caaacctgtt attttacaca ttctcaaatg aaagtcccta tcaggccacc tgctgaagtg 28080

tacgtgtgtt aaatttgagc catctcacat gatagccaga tttgtttcag gaaaacatcc 28140

tgctttccaa ggatttagaa gggtatgttt ttcactggtg attcaggcaa catgcatcag 28200

atttctggtc ttcaaggagc catattctca gaagggagat caaggaccac gctgtgatta 28260

cttctgactt caggagccac tttctgtcag tgaaatttct ctttttgctt ctagcaccga 28320

gtggatttcc ttcagctgat gattgactct cagaattcaa aagaaactga gtcccacaaa 28380

ggtaaccaga gtgtttctga gggctacttg tggggcactc agagggaagg ccttgttctg 28440

aaaatgtgca ggaagtattc caggatgatg agaatttctg ccacatagca gaacgacaca 28500

tgtttgaatg ttataagtgg tagttggagg cactttctag aggcatgcag gcatagatag 28560

ccatgttcta agagtaaagg gcaaccctaa gcaaacctgg catgctagaa agtcagtctg 28620

cggtctgtgg atcacctaca tcagatcaaa tgccaattct cagcctcctt cagatccact 28680

gaataaaaat ttctgcctag aaatttatta ggttgctgca aaattaattg tgggtttttc 28740

cattactttt aattgcaaaa aaatgcaatt aaaagtaatg gcaaaaacca caataacttt 28800

tgcagctacc taatacatct aacatccaat caggagccac gctgttccaa aggggtgatt 28860

ttaactggca gtacttgtga aagtgtgttc accaggtaat ctactgcaag tattttcact 28920

ttggaatgga tagtaactgt ggggaaaacc tctgagaccg tgtaaatatc ctctttgtct 28980

tcaatgttcc acctacgagt tttacaaccc atgtatgttt tttactgaag tcactattac 29040

tatgacagtg gcaaaatgat gaccatggtc aattacaagc caccaagact tggcaaccat 29100

ctcacaaaat tcctgaatat ttaactattg gttctagaga gcaggactgg gcttactcca 29160

gcatactgct ttaaatatat ccatgtctac atccactttt gtctgtatgt ctatgtatct 29220
atctatgtat ctatctagct atgtatctat ctatctatct atcatctatc tatctatcat 29280
ctatccatct atcatctatc atttatccat ctatcatcta tctacttata tattatctat 29340
ctatcatcta actattcatc tatctatccc aatataactt gctgtgataa aggaaatagt 29400
ctattgtttt actgtttcat atagaaatca ctagacacat atggctattg agcactggat 29460
atgtggctag tgccattgaa gatcaatttt aaatggtatt tcagtttaat ttaataaaat 29520
ttgattttaa atagccacta gtgggtagtg gctaccatat tggacagcag agctctaaac 29580
tttgagatta tagttcaatt tcacatcagt atcatcaggt tcatgataac tgaatactat 29640
gattaggtag ttgaatttac ttataactgc atcacagaag tcttcactgg taaatcacag 29700
ctctgtcgac ctttctcaca ctcctttcat attggttttg gttgtgaatt acatggttgg 29760
agcaggcatt atatttattt ctatgttcca ggtctctaaa ggtcctaatc cagtcctgat 29820
caaacagacc agtgatggac catcctgagc ttctctcagg agagaaatca agaggggccc 29880
aacttgtaat cataggagct tatgctattt taatgccatc catcagacta caatcaatta 29940
ccactcatct agctttttgt ccatctctca ttcttgtaca tcctgagata gtcaattctg 30000
agaactgtag cctagatcta tcacctgatg cctctcaaag atataatccg tgcttctcaa 30060
gctaggctat gcacacaaat cactgcatct tgtgaaagtt cagattttga atcagtagtt 30120
caagggtggg gtttgagatt ttgcatttct aaatgagctc tcaagatgct tctgacccat 30180
ggaccacact ttgaatacca agaagtggtc tgtagaccaa tattggtccc ttaagttccc 30240
tcaaacatat cttcgggaaa cgtcctttga ttttccctac atttaaccat tagtgttgca 30300
aattctctca aagtttgtca agatatattg tagctaaaat aaattacatt tttcttgggg 30360
gagagtacta cctcatatta acttacaata aagtactttt aggatcattc aaggaacaca 30420
cccataacac tgagtatgtt atgcggaaat gctctctctg gaaattacac agctgtgcag 30480
gtggcggggg tggcatgagg aggagtggat ggcccacatt ctcgaagacc ttggggaaaa 30540
ctggattaaa atgatttgcc ttattctggt tctgtaagat acacatcaga atgaaaccac 30600
ccccagtgta cctctgaatt gcttttctat tcttttccct tagggatttg agggcttcac 30660
ttagatttct cttcatctaa actgtgatgc cctacattga tctgatttac ctaaaatgtc 30720
tttcctctcc tttcagctct gtccgatctg gagctcgtgg cccaatcaat tatctttatt 30780
tttgctggct atgaaaccac gagcagtgtt ctctccttca ttatgtatga actggccact 30840
caccctgatg tccagcagaa actgcaggag gaaattgatg cagttttacc caataaggtg 30900
agtggatggt acatggagaa ggagggagga ggtgaaacct tagcaaaaat gcctcctcac 30960
cacttcccag gagaattttt ataaaaagca taatcactga ttctttcact gactctatgt 31020
aggaaggctc tgaaaagaaa aagaaagaaa catagcaaat ggttgctact ggcagaagcg 31080

taagatcttt gtaaaacgtg ctggctctgg ttcatctgct ttctattact acaataatgc 31140
taagtaaaaa acctccaaaa acctcagtgg catctaacaa taagcatttg ttgctcacac 31200
tcatttcaat tggttttggt tgtgaattac atgtttgcag caggcaccat agtggtgtgt 31260
gatgtcccct tagctgtatc cacatatgga cacaggaatt ggctcttttt atctcttttt 31320
attttcttgg ttacagacat gtgacttttt tttttgaaag gtaacaatca ctttctcata 31380
tgttatttga tgctagtggt catagcctat agtcacattt gtttcaatga gaaagaaaaa 31440
ccagtacacg gttatgctaa ggatttcagt ccctggggtg agagccgtct cgaatgtctc 31500
cccacttcat aactcctcca cacatcatag ttggatagtg agctctgctg atattggcag 31560
gacttgctct ggtctggctg tagtctgacg gagcctggcc ctgggtgtgc tgtgcaggct 31620
gactcagctc tccccacacc tatctcatgt tccagtcagg cagtaactgg tgaagaagcc 31680
aagctaggaa ccaggatatc tggctcctga gctaaagtct taaaacacta tcatattgcc 31740
ttccaaatat aacaccaaat actaggtgca tatcaccctc actgttttca gacctctgcc 31800
aaaattggga ttctttgtgg tatgaagaga cacggctttg gggctggccc ggctgtgaca 31860
gtgaggtgaa cacaaaggga tgttcttcag agattacagt ccagccctga agcaacaact 31920
aggagactga ttgagcaagt gaggacaggg ctgtgtgggg ttctatcctc tttataactt 31980
ccactagcac tgaaatcgtg ttctctggtt acatccaacc agagccttct ttgtcatttt 32040
tgggatagaa agggactagt ttatcctcaa attatttatg gagattttat ataatatagt 32100
gtttctctcc acattttctg tatataacaa aagtcctcct tttagtgtgt gtatacacat 32160
atatatacac atatatatgt gtgtgtgtat gtgtgtgtgt atatatatat acacatatat 32220
acacggttat gctaaggatt tcagtccctg gggtgagagc cttcccgaat gcttcccacc 32280
ttcataactc ctccacacat ctcagtgggc cactgagcac agcaatgggc atgacagtta 32340
ttaaaacact ttataaatgc ttcgatcctt taccagtatg agttagtctc tggagctcct 32400
aatacttcat tagtactgca tggactgagt taaaagttaa ttcaaaatct caatttatcc 32460
aaatctgttt cgttctttcc aggcaccacc cacctatgat actgtgctac agatggagta 32520
tcttgacatg gtggtgaatg aaacgctcag attattccca attgctatga gacttgagag 32580
ggtctgcaaa aaagatgttg agatcaatgg gatgttcatt cccaaagggg tggtggtgat 32640
gattccaagc tatgctcttc accgtgaccc aaagtactgg acagagcctg agaagttcct 32700
ccctgaaagg tacaaggccc ctgggaaggg agccctccct gaaccagcct ggttcaagca 32760
tattctgcct ctcttaatct acaggacagt catgtggttg tataattatt tgcttgtatt 32820
tttatattta gagatttttt taatcatcaa attgattatt gtcacacttt acaaaccata 32880
gactagaaaa aagaaaacta cagtcatcca caattccaac aacttacgat gaaggtcatc 32940
agttatgtcc ttatgggtca tcagtgtcca aaatgtaagg actcttttaa aaacacatga 33000

tcacaatgct attattatgt cccccaaatg aatatttttt tcataaatat aatcaaatat 33060
ttaggaataa cattttaata aaaaacatgc atctaatctt caaagaattt tatagcttac 33120
tggaacagat agacaaagaa agcagggatg atactgcatt acatcggtac agtagcatca 33180
tatgcctgtg taaattatct gacttcaact attctatgga ggtgtggggg agaaagaggg 33240
agagatggag agaagaagaa ggaggagaag gagggagaag acaaggtaag gaggagaagg 33300
aggagaatta gaaaaacaag agaggagatg agaaggaaag tgcaaaataa caattttgaa 33360
atagtacaag acaatttccc cttctccttc ctcatgacca atgtaagtgt gacttgaggc 33420
aggaacctac ttttccatca gtcagtccca tcacttatgt gccttttata gtgtggacac 33480
atcaccaccc tgaatataat ttcagtgttt agaaataagt attctttgca acactattta 33540
tctcatctca acaagactga aagctcctat agtgtcagga gagtagaaag gatctgtagc 33600
ttacaattct catagcaaaa taagcatagc aggatttcaa tgaccagccc acaaaagtat 33660
cctgtgtact actagttgag gggtggcccc taagtaagaa accctaacat gtaactctta 33720
ggggtattat gtcattaact ttttaaaaat ctaccaacgt ggaaccagat tcagcaagaa 33780
gaacaaggac aacatagatc cttacatata cacacccttt ggaagtggac ccagaaactg 33840
cattggcatg aggtttgctc tcatgaacat gaaacttgct ctaatcagag tccttcagaa 33900
cttctccttc aaaccttgta aagaaacaca ggttagtcaa ttttctataa aaataatgtt 33960
gtattaataa ttcttttaac tgagtggtct gtatttttta aaaagaatat gcttgtttaa 34020
tcttttacta atttgttctc tgggccaaag aatcaattag gcccatctgt gatctttaag 34080
ggtgcttcag ttctggagtt caaaagctgt agcatcaaaa acatcatgta aagcccatgt 34140
agattagcat ggcataatta tctgcagtct ccttgaactt gagcaaagtt acattcattt 34200
caagtcgatt ggaaagatgg ggaagtattt ttgcacagtc atgaagtgta atgattacct 34260
tgttgtgact tttgaatgct gctcttccca accagaactt ggagaagctt tctcatgaga 34320
gtggctccca accactagct gtacattgga atcaccaggg agctttaaaa attcatgatg 34380
tctgggatat cacagaaatt ctaaactaat ttgcccagag tgtggcttta aaagcttccc 34440
cattgcttct catgtgaagc caaggttgag aatgactaat ttaaggcatt tctggtggat 34500
ataaaggact accacagtcc aaggccatcc tgactgacct caccttccag gtgcctagct 34560
ccatccagct gggctccttt tcaacccaat tataactcta ttaatgttgt tcccagccag 34620
gcatggtggc tcatgcctgt aatcccagca ctttgggagg ccgaagcagg cggatcatga 34680
ggtcaggaga tcgagaccat cctggctaac acggtgaaac cccgtctcta ctaaaaatac 34740
aaaaaattac cctggagagg tggcaggcac ctgtagtccc agctactctg gaggctgagg 34800
caggagaatg gcatgaaccc cagggagcgg agcctgcagt gagccgagat tgggccactg 34860
cactccagcc tgggtgacag cgagactctg tctcaaaaaa aaaaaaatgt tgttcccttt 34920

ctcctcattt tgttcttatc tttcaagtcc tagttcaatc cccaagcccc tccaaagtgt 34980
cttctcctcc tagtccaggg cccatttact tctctgctct gttattggat actggaggct 35040
attatcataa atttgacaat ttgccattaa atcattgagt tttattctct atattttctt 35100
tgtatctaaa atgtcttccc ccctccatta acaatatcct ctcattttat tccttttaa 35160
aatatcccag tggtgccttg caagggactg tatctaatgc aagcatttgg taaatgttta 35220
aggagtgatg tgcagttgat ggcttgcata catatattaa gctatttaat gtgaaccttt 35280
aaacaaatgc cattcgtgca tatgcatgtg tgtgtgtgtg tgtgcacatg tgggcatgca 35340
tgtctgtctg cagtgaaaat atattcaggg tttttgaaaa tttttaaata ataaggtatt 35400
atatttatag aaagatttga aatattttct ctgaagaagt taaagaacag acgtcattga 35460
ttcatattaa acaataccct ataaatctta tttctaggtc tcatgtattt attattcaat 35520
tccacccctt aagtgggctt tctatatagg agaggaagaa gacagaaata gtttccatat 35580
tatttccata ttccatatta tttgtggctt taggccagca gtgtagctgt attatatgtg 35640
cccagacagg ggactcagcc ctgaataaaa gtggtcctct ggcacacctg ggatggggaa 35700
ggtactcctt ggtaagctcc caacctggca cttcttgatc tccctggcaa ttttcttgcc 35760
cattactcca tggagatcag aatatcactc tgttgtgtcc cctcaacacg gaaggagtgt 35820
ctcaataaga atggggctaa aagttgagtc caaacactgt aggaattgag aggttcccca 35880
ccttgcacta cccttggaag ccaagagaag atgttaaaaa taaaatggta atgcttcctg 35940
aaggtgtctt cccatcttta cactggatgg gttcaattgg gaggaattac tggactctgg 36000
aagttgaaga ctgtccatat aattaaaatg tacaataact acccaggttt accttgcaag 36060
tttcaacata cacaaaatta actttatatg actcttcaaa aacagtttgc catcatacct 36120
aataatctgg tttaaatttt aaaaactcat ccattttact taaaatttaa atcaaaaaag 36180
aacacaggtt tccatgaatt tgtctcaggc ctggcacaga atagtactcc ataaatattt 36240
tgttaaatga tagatgatga atgctctcac tgtccaatct tcacacatct tatagactaa 36300
gtataaagaa tccaagattt atagtgctga aagtagtttt tatatgttta caaagcatta 36360
ttgtcattac tgcatttttt ttgcccatta ctccatagag atcagaatat cactctgttg 36420
tgtcccctca acactgaagg agtgtctcac tcactttgat gctatacttt ctacttttgt 36480
ttatttaatg cttctcaata tgcttgttta actgttgcag atccccctga aattaagctt 36540
aggaggactt cttcaaccag aaaaacccgt tgttctaaag gttgagtcaa gggatggcac 36600
cgtaagtgga gcctgaattt tcctaaggac ttctgctttg ctcttcaaga aatctgtgcc 36660
tgagaacacc agagacctca aattactttg tgaatagaac tctgaaatga agatgggctt 36720
catccaatgg actgcataaa taaccgggga ttctgtacat gcattgagct ctctcattgt 36780
ctgtgtagag tgttatactt gggaatataa aggaggtgac caaatcagtg tgaggaggta 36840

gatttggctc ctttgcttct cacgggacta tttccaccac ccccagttag caccattaac 36900
tcctcctgag ctctgataag agaatcaaca tttctcaata atttcctcca caaattatta 36960
atgaaaataa gaattatttt gatggctcta acaatgacat ttatatcaca tgttttctct 37020
ggagtattct ataagtttta tgttaaatca ataaagacca ctttacaaaa gtattatcag 37080
atgctttcct gcacattaag gagaaatcta tagaactgaa tgagaaccaa caagtaaata 37140
tttttggtca ttgtaatcac tgttggcgtg gggcctttgt cagaactaga atttgattat 37200
taacataggt gaaagttaat ccactgtgac tttgcccatt gtttagaaag aatattcata 37260
gtttaattat gccttttttg atcaggcaca gtggctcacg cctgtaatcc tagcagtttg 37320
ggaggctgag cgangtggat cgcctgaggt caggagttca agacaagcct ggcctacatg 37380
gttgataccc atctctacta aaatacacaa ttagctaggc atggtggact cgcctgtaat 37440
ctcactacac aggaggctga ggcaggagaa tcacttgaac ctgggagcgg gatgttgaag 37500
tgagctgaga ttgcaccact gcactccagt ctgggtgaga gtgagactca gtcttaaaaa 37560
aatatgcctt tttgaagcac gtacattttg taacaaagaa ctgaagctct tattatatta 37620
ttagttttga tttaatgttt tcagcccatc tcctttcata tttctgggag acagaaaaca 37680
tgtttcccta cacctcttgc attccatcct caacacccaa ctgtctcgat gcaatgaaca 37740
cttaataaaa aacagtcgat tggtcaattg attgagcaat aagcctaaaa gcactcattc 37800
cttttctttt ccaaattctt cctttatttt cccttcctga ataatttagt cctaaagcca 37860
ttaggtgggt ggcagccaga tggtggccac acattaaggt agagaagaga gagtcatggt 37920
ggctccaagt cagagaccaa ggaggttcat gtggagagac atcctggcct gggtgtggga 37980
gtccaagcaa gcagagaagg ggtcgacgca gaggggtggc ttgcaagagc agccagagcc 38040
taaatagggt atggagaacc cacatgaggc gaggagggca tccatgagtg ggaggggttg 38100
ggtgaggttt ggctacataa aggggattga tcaaataagt aaatgtatta aggatgatag 38160
aagccaggct tctcaccttt gcagaaggga gtcatggatt cagaaaggga gaaaactagc 38220
atgaatccta tgaaattaga ttggaatgga tgtaaccgtg tatattcata cccttgtaga 38280
tagatagatg ggtagataga tgatagatag gtaacagata gatgacagat aatgagatag 38340
atagatgtaa atgtatgtct gtatttgtgt gtgtgtacaa aaaacatata ttccctactt 38400
ctctccactg atagggctag gtaacaatga catttcaata gcaatgaaca cacttagtgc 38460
cccgatcttg gcttatgaat accattttcc actgaaggga accagagctc tttagagaaa 38520
tggctgatgc cagggcaaga attaagaatg ttcaagataa gtttaggaca cattttgtgc 38580
caggaagcaa gaaaattttc aaataatttc caagtaatct ttggaaatga tacttgaaaa 38640
tgacttccaa atgacatttc caaatgactt gcaaacgatt tccaaatgat atttggaaaa 38700
acctaaagac tccatcaaag aactattgga actgataaac acattcagta aagttgcagg 38760

atacaaaatc agcatacaaa aatcagtagc atttctatat gccaatagtg aacaatctgg 38820

caaaaataaa aaagtaatcc catttacaat agccacaaat aaaactaaat acctagaaat 38880

taacttaatc aaagaagaga aaggtctcta caatgaatac tgtaaaacat tgatgaaagg 38940

aattgaagac acaaaaaagg atatttcatg tttatatatt gtgagaatca acattgttaa 39000

aaatgtccac actactcaaa gcaatgtaca gattcaatgc aatccctcaa aataccaatg 39060

acattcttca a 39071

<210> 40
<211> 26865
<212> DNA
<213> Homo sapiens

<300>
<308> http://www.genome.utah.edu/genesnps/
<309> 2002-06-05

<400> 40
ggctgcaaat ggccttaaaa atctgaacaa catttgaaaa ttctgagtaa tgggcaacca 60

ggcagtctgg cttatgaggc ctggccagct cttcttcatc atgaggcccc ctacctgctg 120

ccttcctgcc taattccagc agccttcact ccatccttac taaacttgca gacagaccac 180

tcccagagag tgggacagat gccatcagat gccatctccc acctctgtga gcctcaacta 240

acaactcctg tttggcccat ctcttctata atgattgaca ccaagaatgt ctgctacctt 300

ggggctgtga tttcatctgg taatataaaa aaaatttttt ttttgagagt ctcactctgt 360

catccaggct ggagtgcagt ggcatgatct cagctcactg caacctgtac ctcccgggtt 420

caagcgattc tcctgcctca gcctcccaag tagctgggat tgcagatgca cgccaccatg 480

accagctaat ttgtgtattt ttagtagaga tggggttttg gcgtgtcagt caggctggtc 540

ttgaactcct ggcctcatgt gatccacctg cattggcctc ccaaagtgct gggattatag 600

gcgtgggcca ctgcgcccag cccgagaggt aaatttttttg aaataagctt tagtggaaca 660

atcctgaaga ataacacaag aggaataaca ggttaccagt aaggtgtcag ccaatttgtt 720

ccagtcactt ttgaatccat gtcctataat ctaaaattta gttctctttc cctaagctga 780

gagctttcta tcatgtcagt atgtatgtta tgaagaaaag gagacttagg tgagatgttt 840

gtatttatca caactgctgc atcaattgcc taggacttca acagcttcat ggaagtctgg 900

gaaatgttca ggcataaggt tattgcctta gctgactgaa aattgcccca tacagtggta 960

catatcaacc cttagtgagg ccttttaaaa aacaaacagg ttgaaaaata gattaaagta 1020

ggcaaataca gcatctgtct ttagagctat caactcagga attctctcaa ttttttttt 1080

ttttttttt ttttgagat ggagtcttgc tctgtcaccc aggctggagt gcagtggtgc 1140

aatctcggct cactacaagc tctgcctccc aggttcacac cattctcctg cctcagtctc 1200

cggagtagct gggactacag gtgcccgcca ccacgcccgg ctaatttttt gtacttttag 1260

tagagacgga gtttcaccgt gttagccagg atggtctcga tctcctgacc ttgtgatctg 1320

ctggcgtcag cctcccaaag tgctgggatt acaggcgtga gccaccatgc ccggccagga 1380

attctctcaa ttatgaaatc ttgcagagaa gttatttttc tttctcaaaa tccagatgat 1440

gacaatattc cttactccag atctggcatt ttttcatcat cactgtcttg tgaatgatca 1500

tctgctccat ctgctaaatc tacatcctct tcaccaccca tgtggttcat catctcagag 1560

aaataatcaa aatcagacat ggcttcatct gaaccatctt cccagtcttt ccaatgattg 1620

gagtccacac taagccagtt aagctttgcc ctttgttttg ttaaccttgg ccatgactgg 1680

ccccattttc ctttttgtaa acaaacaaaa ccgatctgtc cattctctta tgcttgaaat 1740

catttggatc aatacagtga aaaagattga tgccatataa atgcttaaaa tgatcacttc 1800

caggaagtgg cagtacaagg gcttctgcac ggatagcaga gcagtggtcc cgaccacagt 1860

gcatgccctg agctctccgc ctcccctgcc tgtctgcgag gtggcagcag tgccacaagc 1920

agcccacggc agggtggaac acccacatcg acaacctcgt ggtggaaggg acctgtagga 1980

tgcagccatc gtgggctaca aggacttgcc ttccatccag gccaccatcc ctgggaaaac 2040

cttcatcaac gtcaagccag ctgaggttga tgtcctggtt ggcaaagact ggtcaagttt 2100

ttttgtgaat gaggtgacac ttgggggcca gaaatgttct gtgatctggg acctactgct 2160

gcaggatggg gaactgacct atctttatac caagagcacc gatggagccc ccaccttcaa 2220

tgtcactgtc accatgactg ctaggatgct agtgttgtag gaagtcaggg acccaaatgg 2280

agggatgggc tggaggcatg gcagaggaac agaaattgtg aagatttcat tttaatatgg 2340

acatttatca gttcccaaat aatactttta taatttctta tgcctgtctt taatctctta 2400

atcctgttat cttcataagc tgagggtgta tgtcacctca ggaccactgt gataattgtg 2460

ttaactgtac aaattgattg taaaacatgt gtgtttgaac aatatgaaat cagtgcacct 2520

tgaaaaagaa cagaataata gcgattttta gggaacaagg gaagacaacc ataaggtctg 2580

actgcctgtg gggtcgggca aaaagagcca tattttcttt cttgcagaga ggatataaat 2640

ggacgtgcaa gtaggaaaga tattgctaaa ttcttttcct agcaaggaat attaatatta 2700

ataccctgtg aaaggaatgc attcctccgg ggaggtctat aaacggccac tctgggaatg 2760

tctgtcttgt acagttgaga taaggactga gatatgccct ggtctcctgc agtaccctca 2820

ggcttactag ggtggggaaa aactctgccc tggtaaattt gtggtcagac tggttctctg 2880

ctctcgaacc ctgttttctg ttgtttaaga tgtttctcaa gacaatatgt gcaccgctga 2940

acatagaccc tcatctgtag ttctgctttt gcccctttgcc ttgtgatctt tgttggaccc 3000

ttatcagtgg ttctgctttt gcccctttgtc ctgttccctg agaagcatgt gatctttgtt 3060

agacccatat tagtagttct gctttttgcc ctttgaagca tgtgatcttt gtacctactc 3120

cctgttctta cacccccctcc ccttttttgaa acccttaata aaaacttgct ggtttgaggc 3180

tcaggcgggc atcacagtcc tactgatatg tgatgccacc cccggtggcc tagctgtaaa 3240

attcctctct ttatactgtc tctctttatt tctcagccag ccgacactta tggaaaatag 3300

aaagaaccta tgttgaaata ttgggggctg gttcccccaa tatctggcac accaatgtgg 3360

ttttctttct cctaattgca tgtgggaacc tgattccctt tggtaggtgc ggagaaacgt 3420

tcattggtct ggtccacaga aatgcttgtt cagctctctg atgattggta agttgtctgt 3480

gtattgtcca ggctaacttt gggtcactca gagtctaaac attatgctta tctctgccat 3540

attaaactcc tgttaaaaca ggggggagtt tgggtaccca tggaaaatat ggtcacccta 3600

ttcagggcag tggaagaaca ttgtcctttg tttcctgaaa agggaacatt agacgtggaa 3660

ctatgggatc gtgttggtgc aaaattccgg gaactggtcc caacaggaaa ttatgttccc 3720

gtcactgttt ggggtgactg ggccttggta tgtgccgtcc taatgacata ccaatcccat 3780

cacccccctgc agttaccaca gttttctgaa tctggaaacc ctccacctct tcctcaacct 3840

tcctctcccg cacggccttc gttacctgat cagcctctcc cttcgcctac tccttcccca 3900

cctgaggata ttgaagattc aatatctaac tccagtgact ttggcttaac gtcacccccct 3960

gatgatctta tttcttttca cgaacagcca gtacttgtag ctcccacggc cccgacttgg 4020

acagcccagg actgtatcta tgctaactct tccctcttca aacctttgca gcctttgcct 4080

ccggagccat ctaatggctc cggaactaaa ctacaattta cctgtaattc tgcaggccct 4140

cccccatcca ccacagcccc tcaccctcct gtcatttcgg ttcctcaact ggtcactttg 4200

ccatccactc aacctgcttc tctgtaccct tcttcacatg tggacacccc tgccactctg 4260

gttgcacagg attgggcaat aatcaccagt atgcttctgc ctcttctgct cctctggtgc 4320

ccctttctca cgctctcata ctggtccaac ctcctcagcc tcagtttccc ttatctacac 4380

ataattttcc tgtcacttct gtgccaactc tgtctcatgt gcctgttgtt gaaatttcca 4440

tgcaatgctt attacgccaa aacaaacaag tggattagag gcgtgggctt atccgttcat 4500

gctggaacct tgcaatgctc aaggggtaca agtgcatcga taggcgctgc tcaatcttac 4560

ctttttaaaa gaattcaagg atgcttgtac tcagtatggt cctacttctc catatgttaa 4620

aatggtatta cagactcttt gtactgaggt cattttgctt cctttagact gggacttttg 4680

gcaaaagctg ttctaactcc atctcaacat ttacaattct gtacctggtg gtcacgggag 4740

gcccatctgc aggctcagct aaatcgggct gatggcattc taattactca ggctcagctc 4800

acaggctcca ataattactc tgacactact gcccaattag gctttgatgc tctcaccgtg 4860

gaacaagtaa caaaggtgtg tatgagagct tgggataaat tacgcgcccc aggccaagct 4920

cctgtttctt ttactactgt taaacagggt cacaatgaat tatatcctga ttttttagct 4980

aaattacaag atgctgttga aaaatctgtc tctgatgagc acgctcaagg tattcttctt 5040

cgaatgttag cttttgagaa tgcgaaccat gagtgtaaaa tggccatgca ttccgtccaa 5100

caacaaaatt tacctgatcg tgaggtgttg cctgagtata ttaaatatga aggcattgga 5160

tcagacacaa agctattctg tgcccacaaa gctattctgt gggcacgggc catgaaggac 5220

ggcaatcaaa ctggctcgac tgattctttt cttggagcct gctataattg tggtcaactt 5280

ggtcatactc gaaaaaattg cacagttaaa aacttaaagg cagccaagcc ggctcaaaaa 5340

acacagccaa atgctcctgc tactgtttgc ccttgttgtt gtaaaggtaa acattgggca 5400

agtacttgcc actctaagtc tgatatagat ggaaatccct tgccacagaa ccagggaaat 5460

gggaaatggg gccagtccta ggccccaatt tcaaatggga cacctcagac tcagacgaat 5520

gttgcctttc tgcttcaatc ggtcccaacg cagcccccag cacaaacaaa tttacctaca 5580

gccaacccag atgtgtccca gcctcttctt ctgtctcagt acaacgctta tctatgctcc 5640

agagtaaggg gaggggcggt caatctctgt agtaccattc ctctaaattt actacctaat 5700

tctttgcctt taattcccag accaatacct ggaaacctgg aacgattata acatggggaa 5760

gagggtatgc ttgtgtttca ccaggagatc atcaatcccc tgtctgggtg cccactagaa 5820

gacttaaact tcatgtgaat actgacaata aaaaccacag ggaagagacg tccacgtcag 5880

agaccaccct catacctggt gagatctgtg ccaactcctc agaaactggc acgccaaatc 5940

aaaatgggtc tggttcaatc ctccctaatg gcaacagaaa cccctctaac taatcccact 6000

tctcctaatt ccctttcttt ttctccttac gaacctaaaa atctcaccat ttctattagc 6060

ctgaaaataa catcccctta ttcttctatt cctccttcag cactggatct tgcttacaat 6120

aggttttatt taataattct cttccttata ctttctgtct caccagtttc ccctcacatt 6180

gatttacctg ctacacaaaa ttattcttgc tgggcttatg tgccttttcc tccacttatt 6240

caacctctca cctggatgga tgctcctgcg gaaatctata ctaatgatag tgtgtggatg 6300

cctggagcta cagatgaccg ttgccccact caaccaggaa aagaaggcac tgcatttaat 6360

gttcctacgg ttataaatac cctcctctgt gcctcggaca tgcaccttgt tgtatccatc 6420

tagaaactca agtctgggct gcgtaccttc tggagagatc agccacaggg gaacggggac 6480

atttggtctc cagcctctcc ctttctcctt taagacaaat gaaaggggga gtaataggag 6540

ataccccctа ctttcaatat aaacctgtag gaaaaccatg tcctaaaatt tttgagggcc 6600

catctaaatc tttaatttgg gaagattgtg ttaattcaca tgcagtacta ttaaaaaatg 6660

actcatatgg tttagtaaga gactgggcac caaagggcta tttgaaaagc agttgctctt 6720

ctgctggaag ggaatgcctg gaggctactt gttttatttc ttattgggag gacgaggatc 6780

atcatcctac tttgcatagg aggttcagct cattctgtcc cttaaaatgg gaagataaga 6840

gcattacccc ctgccacccg aggcctctta tgatatcccc cattctgagc ccagaacacc 6900

cagaactttg gaaattggct attgccatgt ccagactgcg agtatgggaa ggggaaactt 6960

ttctttctgt tgtccccact accacccctc acatccgtga ttctgaaacc catgataaat 7020

ccccttttgga ccattttcct ctttttgatg ccagtcctcc tttatgggac tctgattggc 7080

attatgataa ttcttctgga cccaggtatg tccccctacc tcttcagaat ccccgggcac 7140

ctcggattgc ttctttacgg catcaaacat tgggcgttgc caccgccact cctccccctc 7200

ggtatcaacg tagattcaaa cattctgctt tgtttacctc cagcctgact attatacaga 7260

gttgtgttaa gcctccttac atgctgttag tgggaaatat caaaatttgg atgaacaatc 7320

aaaccgtcca atgcattaat tgtcatttat ccacttgtgt taactcccgt tttgactcag 7380

gaaaagtgta atgttggttc gagcttgaga aggaatctgg ataccagtaa ctttacccag 7440

aacttgggaa tcttcccccc cagtacattt aattaatgaa gtgttacaac gaattctcaa 7500

aagatcaaga gatttgtttt cactttaatc actgtgatca tgggcctaat tacagtcact 7560

gcactggcca ccactgccgg agtggcatta caccaatcta ttcaaatggc taattttgtt 7620

aatgattggt aaggcaattc cacccaaatg tggaatcctc aacaaggcat tgatcaaaaa 7680

ttagctaatg atttaagaca gtctgttatt tggcttgggg accagctaat gagtctcgaa 7740

catcacatgc aaatgcagtt cgattgcaac acttctgatt tctatagcac accatattcc 7800

tacaacgaga ctgatcatgg gaaatggtca aaggacacct tctgggtagg gaagataatt 7860

tatccttgga cataactaaa ttaaagaaac aaatttttga agcctctcaa gctcatttat 7920

ccattgtgcc tggagctgag gcgttagatc aggtggcaga aagtctttct ggactaaact 7980

ccacaacttg gattaagtct actgggggct ccactgtagg aaattttgga atcatgtttc 8040

tctgtttaat cggcttgttt ttagtgtgcc agaccagtca aagaatcctg catcaaaacc 8100

gagagaacga gcaagccttc atcgccacgg cacatttata taaaaagaaa gggagagatg 8160

ttgcgggaag tcagggaccc tgaatggagg gactggctgg agccatggca gaggaacata 8220

aattgtgaag atttcatttt aatatggaca tttatcagtt cccaaataat acttttataa 8280

tttcttatgc ctgtctttac tttaatctct taatcctgtt atctttgtaa gctgaggatg 8340

tttgtcactt caggaccact gtgataattg tgttaactgt acaaattgat tgtaagacat 8400

gtgtttgaac aatatgaaat tagtgcacct tgaaaaagaa cagaataaga gcaattttta 8460

gggaacaagg gaaaacaacc ataaggtctg actgcctgca gggtcgggca gaaagagcca 8520

tattttcctt cttgagagag gctataaatg gacatgcaag tagggaagat atcactaaat 8580

tcttttccta gcaaggagta ttattattaa taccctggga aaggaatgca ttcctggggg 8640

gaggtctata aacagccgct ctgggaatgt ctatcttgtg cagttgagat aaggactgag 8700

atacgccctg gtctcctgca gtaccctcag gcttactagg gtggggaaaa actccgccct 8760

ggtaaatttg tggtcagacc ggttctctgc tgtcgaaccc tgtttgctgt tgtttaaggt 8820

gtttatcaag acagtatgtg caccgctgaa catagaccct catctgtagt tctgcttttg 8880

ccctttgcct tgtgatcttt gttggaccct tatcagtggt tctgcttttg ccctttgcct 8940

tgtgatcttt gttggaccct tatcggtagt tctgcttttg ccctttgtcc tttccctcag 9000

aagcatgtga tctttgttag acacttatta gtagttctgc ttttcgccct ttgaagcatg 9060

tgatctttgt acctactccc tgttcttaca ccccctcccc tttttgaaac ccttaataaa 9120

aacttgctgg tttgaggctc aggtgggtat cacagtccta ccgatatgtg atgccacccc 9180

cggcggccca gctgtaaaat tcctctcttt atactgtctc tctttatttc tcagccggct 9240

gacacttata gaaagaacct acgttgaaat attgggggtg ggttccccca gtacgctagt 9300

cctgctgatg agcaaagaag gtgttgatgg cattttgatc aacaagaaat gttatgaaac 9360

ggcctcccac ctctggcatt cctagtactg acctatctct cccttccctt ccaccgctcc 9420

ccacagctta gcaccccttt cgttcccata cacatgtaca tttttatttt ggggaccatt 9480

aacccacagc ccttatcgct gccaaaacca catgggctgg agggccaggg ctgcatggac 9540

agtcacacca ctgcacacca gcctggtgat ggagcaagac tctgaaaaaa aaaaaaagaa 9600

gcataaaaga cctttaacag tccctgctac ttgtgaccct cctgaatctg tcatctgtcc 9660

agtgattttg attttgcaac atggaaagtt ccaagccttg actcctgagc ccagatacca 9720

ttcgcactct ggagtcattc aagcatgggg agctcctcag agggtgatca actgacctcc 9780

cttacctagc tcctcctccg gaggtttgcc ctggagttga gccagccctt gaggaggcct 9840

tcactcccac cgcctctctc ccttctggat atgagctcag gcctggctgg gctccaggag 9900

aatctttcca caaggcaaga gataacacaa agtcaaggtg aagatcaggg tagcccttta 9960

aaaggcctcc ttgtgcccta gagttgccac agctcttcta ctccactgct gtctatcttg 10020

cctgccggca cccagccacc atgtgggagc tcgtggctct cttgctgctt accctagctt 10080

atttgttttg gcccaagaga aggtgccctg gtgccaagta ccccaagagc ctcctgtccc 10140

tgcccctggt gggcagcctg ccattcctcc ccagacacgg ccatatgcat aacaacttct 10200

tcaagctgca gaaaaaatat ggccccatct attcggttcg tatgggcacc aagactacag 10260

tgattgtcgg ccaccaccag ctggccaagg aggtgcttat taagaagggc aaggacttct 10320

ctgggcggcc tcaaatggta agtggtgccc atctcctccc tgcccccttc accacccccc 10380

gggattgttc aggtcttcag accatgccta gaatggggct tccagctcca acaacctgta 10440

attcttccca aagtagacta gtgggatgat gtgaagggag tgaaccttca gacccccacc 10500

cagcctctaa attaggcagg aagaattaaa ggaatgtctc ctctaccagg ctgcccagga 10560

ggtgggatgg gaggaccaca gtggtctgag gggtcaagga atcctcactc cactcctctc 10620

tctgagccta gacttctcta atggactgag aaggtgcatg tacagcactt agcctagcac 10680

ccagcacagt aagtgccccc tatacagcca ggattcatgt tacttttcat ggaaaatggg 10740

ggcagtgact actgtcctcc atgaaagctg ctggggagaa ttagcctagc tattgcaggc 10800

tgggattgct gctttcctgg tgctatttcc agctactcag gctcacaggg gcagttttct 10860
acaatgacat ttcagggttg ctgatgagcc tcccactcag cagggccccc agcctctcag 10920
catttttttt ttttttttt ttttttgaga cagagtctct ctctgtcgcc cagcctggag 10980
tgcagtggcc aatctcagct cactgcaacc tctgcctccc gggttcaagt gattctcctg 11040
cctcagcctc ctgagtacct gggactacag gagcatgcca ccatgcccgc taatttttg 11100
tatttttagt agagatggtg tttcaccatg ttagccagga tggtctcgat ctcctgacct 11160
cgtgatcctc ccaccttagc ctcccaaagt gctaggatta taggcgtaag ccactgtgcc 11220
ctgccagcct ctcagctttg atcaagccaa gggttggttt atttttttctt ggaccaatca 11280
gccaggtctg ctgaccaact acctagctcc cacctctgct ggcttcctcc cgggggcaga 11340
gaagatggag aaggctagtc atgtggatct tcagggtcag gaaatggaaa agggaggctt 11400
tggacccttt tgctttgggg ggcacctcta ggaggaggcg gctcggccca agtccagact 11460
gggtagacaa aacatctgca ctctccaaat gtgggcttgt ggctgggtat gcaggcttgc 11520
aatggaaggg taaacctgag tgaggtgagc tgtgccttta gctcagctaa gggctcaggg 11580
aaaagcagag atctgtgcag tcctcagcct ctacaagctc acctgctccc taccctctgg 11640
acaggcatag tttagagagt ttatcccatc cagagttgcc ttcctgtggt cagaaactga 11700
tgagcaaaaa gaagcccaga gggcaccctg tcagcgaaaa gaaccccaat gctgctgcat 11760
tctaattaag ggttctttct ttctccttga tctactgtat ttctgaagga attgggagta 11820
ggaggcctta gggtctgtcc taccaagtcc ttgcagtcat ggtggagtgc agtggggctg 11880
tgcccacatg ggagtcagca tgccaggtac ctgccttctc ctccaggaag gaaagcaggg 11940
accagaggtg taagggcaag agtggggtgg atggtgtgag attcctacag ccttgcctgc 12000
tctctaaagg caactctaga catcgcgtcc aacaaccgta agggtatcgc cttcgctgac 12060
tctggcgcac actggcagct gcatcgaagg ctggcgatgg ccacctttgc cctgttcaag 12120
gatggcgatc agaagctgga gaagatcagt gagtgccagg ctggcccctg gggctggggc 12180
tggatcccac aggagctgct ggagggagag gagggttggg caggggtaag ggttaggact 12240
agagcgcaat gcagcctttt cttggctact gctgccatct agtggccatc tgctatctgt 12300
cccccgctcc tgttaagagg caactggtac agagaggggg taagggtgct gattcatttc 12360
ccaccctcat gccccctctc ccttcagttt gtcaggaaat cagtacattg tgtgatatgc 12420
tggccaccca caacggacag tccatagaca tctcctttcc tgtcttcgtg gcggtaacca 12480
atgtcatctc cttgatctgc ttcaatacct cctacaagaa tggggaccct gagttgaatg 12540
tcatacagaa ttacaatgaa ggcatcatag acaacctgag caaagacagc ctggtggacc 12600
tagtcccctg gttgaaggtg agatgctgcc agccctgcct tcaggttcta gtagaccctg 12660
acattgtccc caatcttcct tccttttttac ttccctgctc cagccgcaat gacccatctt 12720

tttcctgatt acctccgcca cctctacctc ctctgccact taaaaccttt gccatttctc 12780

tgcagagata gatttagcct tttaattatg caccttagta ctccagataa tgaccttcat 12840

ttcttttcca attaccatgt gccagtacta agcattctat acgcattcat cgctgaattc 12900

cccttggaag taggttttat tatccccatt gtgcaggtga gaagcaggct tagcggggtt 12960

aaggagcttg tctgagcctt caggctcatg tctctctcac tcctaagggc tggacacata 13020

gcagagtcag cgcttgatgt ttgattgaat ggggaaggag aggtggagac cacgccctcc 13080

tcccttgttt agaattgtct tcgtcgtcat gataaacccg ttctgtgtcc ccatcttgcc 13140

ttccattctg gctgaaggtc aggggtggag taggaacttc cagagacaga aagctaagat 13200

ccgcctccag gagagactct ggcagctgga gaagcaaaat ggaagaaggg tggatttaac 13260

atttcttttt atttcccaga ttttccccaa caaaaccctg gaaaaattaa agagccatgt 13320

taaaatacga aatgatctgc tgaataaaat acttgaaaat tacaaggtag gtgatagagc 13380

agaagagaat atgagttagg ctaaaagtaa tcacaagagc agggtggagt ccattctaca 13440

cactgtagaa gcttcaaaac caagcagaga acctggcaca tagtaggtgt acaataaaaa 13500

ctgacttaag ggctgggcgc ggtggctcac gcctgtaatc ccaacacttt gggaggccga 13560

ggtgggcaga tcaattgagg tcaggagttc gagatgagcc tggccaatat ggtgaaaccc 13620

cgtctgtact aaaaatacaa aaactaggcc aggcaagatg gctcacacct gtaatcccaa 13680

cattttggga ggccaaggtg ggcagatcac ctgaggttgg gagttcgaga ccagcctgac 13740

caacatggag aaactctgtc tctactaaaa atacaaaatt agccgggcac ggtggcgcat 13800

gcctataatc ccagctattt gggaggctga ggcaggagac tcacttgaac ccgagaagca 13860

gaggttgcag tgagctgaga tcatgccatt gcactccagc ctgggcattg caccaagatt 13920

ctgtctcaaa aaaaaaaaaa aaactgactc aaggagttgg gatcgaaaag tgaggaactg 13980

aagaggatcc tagaagagac ctaacctctc caccaaattt aaagagggcc cggggctgcc 14040

tcctacctcc acaagttcgt aggtcctgcc cagacttgct ctacttccaa gtggaaggag 14100

ccttgttatc tctagtcagg gacagaagta tggcaggagt gtcacagatg gggctccttc 14160

cttattaatg tctcccaacc tcacccaacc caggagaaat tccggagtga ctctatcacc 14220

aacatgctgg acacactgat gcaagccaag atgaactcag ataatggcaa tgctggccca 14280

gatcaagact cagagctgct ttcagataac cacattctca ccaccatagg ggacatcttt 14340

ggggctggcg tggagaccac cacctctgtg gttaaatgga ccctggcctt cctgctgcac 14400

aatcctcagg tgtgcttccc cctcattgat cctagacccc agccagccca atctctgggc 14460

tccagagaaa gggagagcca attctctcag gctttctgtg caggaagact aggcctgccc 14520

tgctccttac ccaagcagta gttggctttg accccagagt agagctgccc catcttctgg 14580

aagccgggcc tgggccccag agccactact gggaagggac tggacaggct cttctcgatg 14640

tcacagttgg attcttctct aagcccttgc ttctcctggg cttacacaca ctagtcacct 14700

ccaacctact ctggtcttca ggtgaagaag aagctctacg aggagattga ccagaatgtg 14760

ggtttcagcc gcacaccaac tatcagtgac cgtaaccgtc tcctcctgct ggaggccacc 14820

atccgagagg tgcttcgcct caggcccgtg gcccctatgc tcatccccca caaggccaac 14880

gttgactcca ggtgtgcctg ccctcccagt gacatctagc cccatgatgc attcaacact 14940

gcttgccagc ccacctggct ccccctaccc ccggcccctg ctggccaacc taaagtcagt 15000

caaccatcaa ctactaaaaa tcatcctgcc ggccgggcac ggtggctcac acctgtcatc 15060

ccaacacttt gggaggtcga ggcgggtgga tcatgaggtc aggggttcaa gaccagcctg 15120

accaatatgg tgaaaccccg tctctactaa aaatacaaaa attagccatg catcgtggcg 15180

cgtgcctgta gtcccagcta ctcaggaggc tgaggcagga gaatcacttg aaccaaggcg 15240

gcggaggttg cagtgagcca agattgcacc actgcactcc agcctgggtg acagagcggg 15300

actctgtctc aaaataaata attaattaat taaatataaa aatcatcctg cccccagccc 15360

cgtggctcca tgtctctacc acctacagac acgcattgac tcatccacag atctgcctga 15420

cttcccagag gagcttcctg ctgccctcag agacatgtgg tctgggatga aaggctggga 15480

gctccatgtt ccaaccagct gcagcacgca cataacatgc gctgcagctc caaacgcaca 15540

cccacataca ctgccagaca ccaaagtcca cagacacagg tgttcagaca gaagcgcctg 15600

ttaggaggga agggatggag aagggctgga tttaggtttg atctggcaga agctgaggaa 15660

aacatgagtg agtgggaatg agggagtaaa gggcatttтc ctcacggcgg aagaatgagg 15720

gggcatgagg ctgagcaagg aagggagtac gaagtcccag acccactttt cctcttccac 15780

tctggagcag catcggtgag tttgctgtgg acaagggcac agaagttatc atcaatctgt 15840

gggcgctgca tcacaatgag aaggagtggc accagccgga tcagttcatg cctggtgagt 15900

ctgtcctgtc ctgcgccctg ggccacacag cgagcctgga ctctgctcca ccaccccagt 15960

acccccttcac ctctgccaag cttgctgcta gaaaactctt ggctccaact atacggacct 16020

gttgacaccc tcatcctgcc atagacttac ccaaactctt cacagctggg tttcccacgc 16080

tcttcttcca accaactgca aattcaccct ccaagaagcc ctctacgcct ctgtctgcca 16140

ttaagtctgt cccttctccc ctcggatggt gctattttca taggttaatt ccatctcttt 16200

tccatccttc ctgaatattt catttcctct gtgtcgttaa gggctacctg aaagcagggc 16260

tgtatctctc cccaggcggg ggttccccca taataaggct acatcctcag atcagggttc 16320

cctgggcagg gccatgtctc cccctcaacc agggcagaac catgcctctc ctccctcctg 16380

ccctaacccc tggctgatgc cactccttgc ctgcagagcg tttcttgaat ccagcgggga 16440

cccagctcat ctcaccgtca gtaagctatt tgcccttcgg agcaggacct cgctcctgta 16500

taggtgagat cctggcccgc caggagctct tcctcatcat ggcctggctg ctgcagaggt 16560

tcgacctgga ggtgccagat gatgggcagc tgccctccct ggaaggcatc cccaaggtgg 16620

tctttctgat cgactctttc aaagtgaaga tcaaggtgcg ccaggcctgg agggaagccc 16680

aggctgaggg tagcacctaa aggctgtaac tcacagcccc tgtccaccct atgtggcccc 16740

acaacacaga tttagagata caacccccca cccttctccg ccattcttcc ctactcccaa 16800

cccactctgc cttctttttc agcttgtggc aatgccagtg atgtgcataa acagtttttt 16860

tttttccata aggtccctga gtagttcatt tatgtattca tttgctcact cattctttca 16920

acaccgattt tattgagcac ctactatgtg ccattcactt tctcaggaca ctcgagctcc 16980

gtggtctctg aagcttacat tctagtgagg gctaacaagt gaataagttc agagactcgt 17040

aagtgctttg aagtcaatca caatttgtgt gatgtgatga gaaaatggca gaggcagtgg 17100

gtggctgctt tgaacaaggg gtcaggaaaa gtgttgcatg ctgagaagca ggtaaaaagg 17160

cctccaggtg ggagaggtca gcatggccag tgaaggggag agtgggccct gatgaggtca 17220

gagtggacat agtggtccgt tcccactgta gctgggatta caggaggcca ggagggaggt 17280

tgggttttat tctaattatg acaggaagtc actggaggat tttaagtatg taagtggaac 17340

aatctgtttt tttgtttttg tttttgtttg agaaggagtt tcgctcttgt tgccctggct 17400

ggagtgcaat ggcatgatct tggctcactg caacccctgc ctcctgagtt caagtgattc 17460

tcctgcctca gcctccaaaa tagctgggat tgcaggcgtg tgccaccatg cccagctaat 17520

tttgtatttt tagtagagat gaggttttgc catgttggtc aggctggtct cgaactcctg 17580

acctcaggtg atccacccat ctcggcctcc caaagtgctg ggattataga catgagccac 17640

agcgcctagc ctgttttttg ttttgttttg tttgggtttt tttgttgttg ttttttgttc 17700

tgttttttga gtgacatggt ctcactctgt tgccaggctg attgcagtgg cacaatcatg 17760

gctcactgca gcctcaacct cccaggctca agtgatcctc ccacctcagc atcccaagta 17820

actaggacta caggcacaca tcaccaggcc tgactaatgt tttacttttt gtagagatgg 17880

ggttttgctg tgttttctag gctggtctca aactcctaag ctcaagcgct tctcccacct 17940

cagcctccca aagtgtttgg attataggca tgagccgctg tgcccagctg gtttgtattt 18000

ctgaaagatc gccgtagttg ctgtgtggag aatgttctgc taagggatgg gagtgggagc 18060

aggagaacag ttaggaagga ggctgttgtg ctggtccagg aaagccagat gttgatgagt 18120

taaaccacgg ccacagcagt ggaaacagtg agaagtggta ggattgagtt tatcttttgt 18180

tttctgtttg tttgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg 18240

tgttttgaga cagactcttg ctctttcaca caggctggac tgcaatggca caatctcagc 18300

tcactacaac ctccacctcc cttgagcgat tctgctgcct cagtctccca agtagctgga 18360

attacaggcg cctggataat ttttttattt ttaccagaga tggggtttcg ccatgttggc 18420

caggctggtc tcgaactcct gacctcaagt gatcccacct cagcctccca aagtgccagg 18480

actacaggtg tgagccaccg agcctggcct gagtttatat tttgaaagta gggcaggccg 18540

ggcgtggtgg ctcgtgcctg taattccagc actttgggag tccgagatgg gtggatcgcc 18600

tgaggtgtgg agttctagac tagcctgccc aacatggcaa aaccccgtct ctactaaaaa 18660

tacaaaaaat tacccgggcg tggtggcagg cacctgtagt cccagctact cgggaggctg 18720

agacaggaga atggcgtgaa ccccggaggc ggagcttgca gtgagcggag atcgcgccac 18780

tgcactccag cctgggcaac agttcaagac tctgtctcaa aaaaaagaaa aaaggaaaag 18840

aaaaagaaag tagggcaaaa gtgttgtttg ttttgatcca aataggcttc actgcatgtt 18900

acctcacagg ttcgaccttg ggggagtgta tgtgacccac agactggacc tgccgttgcc 18960

atccctctgt cttggtctgc aaagaccaag actggtgtgt ccccctttcc tcacccttcc 19020

ctggggtaaa cactgccagg taagggcttc tacagctgtc ttctgcagca gtgcctgggt 19080

tccacctcct tctccccact caaaaacccc aggaagtctg taaaagcttc ctcactaggg 19140

ctgggtgcag tggctcacgc ctgtaatccc agcactttgg gaggccgagg cgggcagatc 19200

acgaggtcag gagatcgaga ctgtcctggc taacacgatg aaaccccgtc tctactaaaa 19260

atacaaaaaa ttagccgggc atggtggcgg gcacctatag tcctagctac tcgggaggct 19320

gaggcaggag aatggcatga acccgggagg gggagcttgc agtgagctga gatcgcgcca 19380

ctgcactcca gcctgggcaa cagtgcgaga ctccgtctca aaaaaaaaaa aaaaaaaaca 19440

aagcttcctc actagaaaat gaagccctga ctcctttata tctggaaact ggtatattta 19500

aaccttggtc attggccagt ctgcaaatga atgtcctgag acatcccgga agaaactgac 19560

ccttttagcc tagagagagg ccccatcccc agctccctgg tgccagccag accagggtca 19620

ggtcatcaac aacccagtcc ttcccctctg actagacaga aggacgtcag cagagcatgg 19680

ctgataccct gcctagctaa gtcttagaga gaagacgtcc ctatagggag caagacaagg 19740

ttttcagtta cgacactacc ttcttcctta taaagagctt tgttaatcag gtggcagtgg 19800

accgttccct actattccct aactcggtct tggccttcat ctgccattta ccctgggact 19860

ttgctaaaga gcctgcagga ggccaagtgt ggtggcttat gcctggaatt ccagcacttt 19920

gggggggcta ggcaggagga tcccttgagc ccaggagttc gagagcagcc tgggcaacag 19980

agtgaggccc tgtttctaca acacttaaaa aaaaattggc cgggcgcggt ggctcatgcc 20040

tgtaatctca gcactttggg aggccgaggc aggcagatca caagatcagg agatcgagac 20100

catcctggct aacacgatga aaccctgtct ctactaatga tacaaaaaat tagccgggcg 20160

tgctggcagg cgcctgtagt cccagctaat cgggaggctg aggcaggaga atggcgtgaa 20220

cctgggaggc ggagcttgca gtgagcagag atcgcgccac tgtactccag cgtgggcgac 20280

agagcaagac tctgtctcaa aaaaaaaaaa aaaaattacc caggcatggt ggcatacctg 20340

tagtctcagc tactcaggag gctgaggtgg gaggattgct ggaccccagg aggccgaggc 20400

tgcagtgatc tgagatcgtg ccactgcact gcatcctaga gcaagaccca atctctaaag 20460

aaaaagaaag aaagaagaag aaggattagt atttcacttt cctgccattc aatgttctgg 20520

ttcaatagtt ggagaatgaa agagtgcata tgtgtgttgg ggggcagagt gagagagaga 20580

aagagatgaa gatatatggg aacctataga cagacaaaca gatatagata gatgtaatat 20640

gcaccaggtc agtatctgtc aaagtgtggc tcacagaccc cttgagccag actcatctga 20700

gaaacttact taagaacaca gactctggtc cctatctttc atgcattgag tacactctgg 20760

gagcagggcc tggaaatctg cattttacag gctatccagg tgaatcttgt acacactgct 20820

gcgcaccccc cccgagtcct caagtgacat tgtgtgagat tcttgcaaac ttgcgatgtt 20880

ttccatccca gttaaaccca cccaccactt ccacagagga cacagatctt ctgctaattg 20940

cttatctctt catcactagt ctacaaaatg cctttcaggc caagcacagt ggctcacacc 21000

tgtaatccca acactatggg aggccaaggt gggcacaacg cttgagctca ggaatctgag 21060

accagcctgg ccaacatggt gaaacctcgt ctctagctgg gcatgttggc gcacacctct 21120

agttccagct actcaggagg ctgaggtggg agaatcgctt gaacccagga ggtggaagtt 21180

gcagtgagcc aagattgtgc cactgcactc caactgggtg acagagtgag tgagagagac 21240

gccgtctcaa aaaaaaaaaa aaaaaaaaaa aaaaaaagcc tttcaaattc tgagcaaatc 21300

tgaaatactt aactttcctc cagccaatct tattcccctc tgctttgagc tgaggatagc 21360

ttgactcgat ccagcaccca gctgatgggg gcagaggaac cgggagaggg aagggacaaa 21420

ctccagtata gcctttccct tgggctcact gtggtgtcag catctctccc aggctgcttg 21480

tgatgggggc tggggtcagc tgcccacaag ctctcctacg gacttcattt ttttttgag 21540

acagggtctc actctgtcac ccaggctgga gtgcagtggt gcaatcatgg ctcaccgcag 21600

tctggaacac ctgggctcaa gagagcttcc tgcctcagct tcctgggtag ctgggactac 21660

aggtgtgtgc caccactctg gctaattttt aagtttttg aagagatggg gatcttatta 21720

tgttgcccag gctggtctca aactcatggc ccctagtgat ccttctgcct tggcctccca 21780

aaattctagg attacagatg tgagccactg tgtcctgtct aaaccttcat tttgaaggaa 21840

actgagggcc attgtgtggg ctgggtatag ggtatgactt gccccagatc acacagctac 21900

gtagcagcag ggctgggacc agaactcaag atttcaatgg tgcatggtgg ggagccagcc 21960

atgctttccc acctgtcccc tgtggtcatg cagaagggct cttgggatat ttggccggga 22020

gagtaccttt caggcaagcg gagtgacctt ttagaaaatg actttatgaa ctttgactcc 22080

tgcccaaact gtgctctccc gtctggaagg ccttttcacc actgatctaa acccacctgc 22140

cttgaggctc agacacattt tttatgactc ctgagtccac catgaccatc cctcttcagc 22200

actcagcttc tgttccttgg tactgaacct aaactgaacc ttggcatctg agcatctgcc 22260

tggacttgaa atgggtgggg ccccccacag acactgtcca cctcctgtac ctctggagtt 22320

caagactgag ccttctcatg ttctttatcc tgcatatcag cacctgacaa atagaagggt 22380

agacaaacaa gagtgatgca ggacaggcaa gccctaaaat tggggcttag cccaggaggg 22440

ttcatggctt cacccagaaa gaattccagc aagcagcagt ggtggtagcc agcaagccgc 22500

agtgcacaga gcagcagagg tactgctcct tgtggagcag ggctacccag aggcagtgtg 22560

cccagaagag caacgcaggg gcagggctgc actcatatgg acatctactt ttaattatat 22620

gcaaattaag gggtggatta tgcagagatt tccaggatga gggtagtaac ttccaggtca 22680

tcaggtcgtt gccacgaaaa gggatggtaa ctcctaggtt ttgccatggc aatggtaaac 22740

tgacatggca cactggcagg catgtcatgg aaagctgctt ctgccccccc acctgtttta 22800

gctagtcctt aatttggttc catgtccgag ccccgcctcc tacctcaaga ggactgaatc 22860

aaatgctcta aatcacttgg ttaattggcc caatgatagt aaataaattc tatctcctta 22920

tgcagaagga agcccagatc tttgacaaaa ctggaaggtc tttgccaaga ccccacagtt 22980

aaccgtctga gcctcagact gtccttaacc agtgatgtga tgataaataa atgtttaaca 23040

accaggtctg ggaggggcgg gggtgtgcgg aatagccttg atttgtaatg tttgctgatt 23100

actgtggtgt agatactccc aacgtgacca attttaaact accaatgtga tgccagtaaa 23160

cagggttgga aagagacaca tagtagcatt atatgttctt taccgttgtt attattacat 23220

agtaaatgcc attatgtagt atttccacca tactgatagg taaatgtaaa taacctcaag 23280

ggcacagata acagtaacat gtagtaaaat aactaggaaa tgatcagttt tgagtatcta 23340

ttacctttgt ttttaatata actcaattgt aggtttaagt tttttaaatt ggctgtttca 23400

tataaacagc tcataaaatt cctgaaaatt taaaaatcag ttctagtgag ctattaagag 23460

ccaaccctcc caggagaaat gggccacgct tgtcttaaag aaaagcagtt cctggctggg 23520

cgaagtggct catgcctgta atctcagcac tttgggaggc cgaggcaggt ggatcacctg 23580

aggtcaggag tttgagacca gcctggccaa cttggtgaaa ccccgtctct actaaaaata 23640

caaaaattag cggggtgtgg tggcgtgcac ctgtagtccc agctactcgg gaggctgagg 23700

caggagaatc actagaacta ggtggaggtt gcagtgagcc gagattgtgc cactgcactc 23760

cagcctgtga gacagaacaa gactccgtct caaaacagac aaacaaaaaa cgaaaaggag 23820

ttcctgggct ggggacagtg gctcaccaca ccagcacttt gtaatcccac cactttggga 23880

agtcaaggtg ggtggatctc ttgagctctg gagttccaga ccagctgggc aacatggtaa 23940

aaccccatca ctacaaaaaa atacaaaaaa ttagccaggt gtagtggcac atacctgtgg 24000

tcccagctgg tcccagttac ttgggaggct gaagtgggag gatcacattg aacccaggag 24060

gtcaaggctg gcagtgagtg cgccactgcg ctccagcctg ggtgacatag caagaacttg 24120

tctcaaaaaa aaaaaaaaga aaaaagagaa agaaaagcag ttcccctgag tctccttgtt 24180

gacaggaggg aaatccttcc ctattgtggg agggtgagag tgagtgaatg ttctatcagc 24240

ctctggtggc cacaaaacct gaggcaaatg aggagccctc tctgcagtca cactcgtaga 24300

tgttagcgcc cttctctgga gggtggggat ccagtcacag aggccgtgca gtggggtggg 24360

aagcgcaacg gataaattgg acccagacca ccccggtgct ctgccccagc tcccgtttcc 24420

tgaccctgga tcttaggccc atcactaact tcctgagcct caatttcccc atggataatg 24480

tgggggaacc taacacctgc gctgcccatc ttccgaggct ctggtgagga tgagaggcag 24540

aaaagagtgt gtgggcagga gagtcccaca cagacgggaa tgcaaatgac tcgaagtcag 24600

gttgcagaga caaatcctcc cagtgttgtc atttacagac tgcgtggcca tggacacctt 24660

aggtggcctt aagccttggt tttcccatct gtaatatggc gggggcgggt ggtagggaac 24720

tgggatgttt gtgtcatagc gttactgtga ggatgaaatg tgaacctatg aaatacattt 24780

agtgccttga taaatattgg gtttctcgtc gttgtctata tccaaaccca cgaaatgagt 24840

ccttctcagg gttttataca aacctcccca aaagccacca gtttggtcag gaggggggagc 24900

gggtgtgtgc agatgagtcc ctccgcagga tggaaccctg gggaacccac cctccccgtt 24960

ccatccctgc agggcccact acagcccctg gcctgccacc tgcccactcc gtccccgcag 25020

agccagggct gatggactgc cgggcagcgg gtggagaacc caaagacaaa ctcacggctc 25080

cagcacaggt gttccgtcac agtttctgtg ggattgggtt tcttgagcct tcttggtgaa 25140

aaaacatgaa atgaagggaa tctgaagcta tggtgaggaa caggcttata acagagtaag 25200

gagaggccag gtgtggtggc tcatgcccgt aatctcagca ctttgggagg ccgaggcggg 25260

cggatcacct gaggtcagga gttcaagacc agcctgccca acgtggcgaa acctcgtctc 25320

tactaaaaat acaaaaaatt agccaggtgt gttggtgggt gcttgttaat cccagctact 25380

tgagaggctg agacaggaga atcacttgaa cccgggaggc ggagattgca gtgagccaag 25440

attgcgctac tgcactccag cctgggcgac aagagcaaaa ctccatctca aaggaagaaa 25500

aaaaagccaa aaacaaacaa aacagagtga ggagaaattt caggtcaaac aaaaatcctc 25560

ttctcccctc acaaacacag aaagctgtac tttcatcacc ttggaggaag aacaaaaaca 25620

ctctttcaag gaaaagagac aaagaagatc caaactgtaa ctcctgagaa ttttacagtg 25680

tttccaaggg gttacaccgt ccctggaagt tgacattggt ccgaatactg gtggcaagca 25740

gcatcacctg tcccaggggt gacgccattt tagcactgaa ttgctcttgg aggtgaagcc 25800

tggctgggtg tgggggggtc tgccccctgg agcaagagga gatagggtag ctcctgagga 25860

aatggtgtct gtttcatctt tcaccatgtt actcttagct caatatattg ttctctagtt 25920

ctccctcacc tttgaaaaga aattacaagg ctcatgcctg taatcccagc actttgggag 25980

gccaaggcag gtggatcgct tgagcccagg agttcaagag cagcctaggc aacatggcaa 26040

aatcctgtct ctacaaaaaa tacagaaatt agctgggcat gacggtgtgc gcctgtagtc 26100

tcacctgctt ggggaggatg aagtgggaag atcacttgag cctgggaagt tgaggctgca 26160

gtgagctgag attgtgccac tgcactccag cctgggccaa aagagaagag aagagagaga 26220

ggaagaagtc acaagttctt caggtggctt gtgagtacct acattacagc tcttcactgt 26280

cctgccttct ggttattaca ttggccttgg agccattaga cctggcttca aatcctagct 26340

ctgccactta ttagctatgt gatcttataa agttagttaa gtcctctgga tgccacaatc 26400

ccattaataa agcaggaata attgcagcct atatacctca gagacctgtt ttgaggctac 26460

atttttttat ttttttgaga tggagtttcg ctcttgttac ccaggctgga gtacaatggc 26520

gtgatctcgg ctcactgcaa cctgagcccc ccgggttcaa gcgattctcc tgcctcagcc 26580

tcctgagtag ctgggactac aggcatgcac caccacacct ggctaatttc gtatttttag 26640

tagagacggg gtttctctgt gttggtcagg ctggtctcga actcccgacc tcaggtgatc 26700

cgcccacctc ggcctcccaa agtgctagga ttacaggtgt gagccaccgt gcccggcctg 26760

aggctaattt tttttttaa atgtagctaa gatgctcaca caagactggc attgtggaaa 26820

ccgtcaacca acaaaacaat aaagacaaat taaattaaaa tattt 26865

<210> 41
<211> 76341
<212> DNA
<213> Homo sapiens

<300>
<308> http://www.genome.utah.edu/genesnps/
<309> 2002-06-05

<400> 41
ttgtataaag tgtaaggaag ggatccagtt tcagctttca acatatggct agccagtttt 60

cccagcacca gcaccattta ttaaataggg aatcctttcc ccatttcctg tttttgtcag 120

gtttgtcaaa gatcagatag ttatatatat gtggcattat ttctgatggc tctgttctgt 180

tccattggtc tataagtatg ttttggtacc agtaccatgc tgttttggtt actgtagcct 240

tgtagtatag tttgaagtca ggtagcatga tgcctccagc tttgttcttt tggcttagga 300

ttgacttggc aatgagggct ctttttttggt tccatatgaa ctttaaagta gtttttttcca 360

gttctgtgaa gaaagtcatt ggtagcttga tggggatggc attgaatcta taaattacct 420

tgggcagtat ggccattttc atgatactga ttcttcctac ccatcatgag tgaactccca 480

ttcacaatta cttcaaagag aataaaatac ctaggaatcc tacttacaag ggacgtgaag 540

gatctcttca aggagaactg caaaccactg ctcagtgaaa taaaagagga tacaaacaaa 600

tggaagaaca ttccatgctc atggaggata taatcttgcc ctgtgttggc caggattagt 660

actcgggttt ctcaggtgat gagcggggcc atagagctcc caagagttta tgtcttttgt 720

tttcagctgc cagggtgggt agagaaaaac cattgagcgc agggtgggtg gggtgggggc 780

gcaggattgg gcaggtctga tgctacttgg gcagggcttg ctgcagccac tgtggaggac 840

agagaggtgg ttcttaagcc aatggtgtta tgttcctagg gggattatgg gtgcctctac 900

tgcattatac atgtcaccag ggaagcgggg gaaaacaggc agtgacgggc ctcactcagc 960

tctcatgcag ccagcaaggc cactcttact cccgccatgc ccctccaaca gcactgagtt 1020

tatatccagg cagcctttga gcagggctga gatctttccc caggctacaa tccttcccac 1080

tgagaaagca agcagggctc tcaggcctcc cttccctgcc tgcccttccc ttcagctgca 1140

gcttctgcaa ttgtatgtgc acttcccatt tgccccccac cccgtttctg cacaggaaaa 1200

ttcgtactca gccaaaatta taacaaagat cagctaggag cttccttcac cctgtggccc 1260

ctccccagtt ctactggctg ccctcccttc ctgaagaatc tctgtgagat gaggccagga 1320

atggtttccc tgggctcccc caggcctcgg cacaaggcct ccagccctcc ctagagaggc 1380

agatgagagt ctttccccaa tggaggtgtt ctctcgctga gaccagggca ggtgccaagg 1440

tgtctgtgga gttcctgggg gcatccgggc agaggggaga aggaggacct gggagagcac 1500

accttcctgc cctcactaga gaggtattta ttaacttctg cgctcctggc cactgactga 1560

attcgtgtct acattatcag ctcatgtaaa ttcattatcc caacagctgg gaatgagctc 1620

cactggatga ggtggtggat gagggcccgg gggctggcag ctatccatgc actgtacaag 1680

ctctcttgac atgggcagtt cagtggaagt gtctacaggg ctcttcccat tgcttcttct 1740

acttttatgt tttgcttggc atcctaaatc tgtttcagct ctgggtaagg ttaaatcctt 1800

ctcctgtgat ctggattttc aggttcccca gtggggatgt gtgttcagag gcaaactttt 1860

ccctgctcac actttgggaa ctcacagttt tttggctgtc tcatagagtt tgcaacagta 1920

aaactgcttc tttcaaaggg tctgtgaatt ctttcagttt tcctggtatg ttcccatggt 1980

agttcttgca gcaaaagctc acagtgtgag tctccacaca ctgttctgtc cattccaagc 2040

aggagctgca tgttagttct gtctgctatc caccattttc caattttgtg atatagttat 2100

gatttttat tggtttgttg ttttgtcttt ctatttagga caagaatagt gtacacactg 2160

cagttagtgt tataatattt agtgtttttc tgtgtactta ctattaccag tttgttttgt 2220

atcttcatat tacttattat tacttaataa gtgattactt actgctcatt aatgtccttt 2280

tcttttgat tgaagtattc cctttagcat ttcttgtagg acaggtctgg tgttgatgaa 2340

attcctcagc ttttattttg gaaagtcttt atttctctct tccatgtttg cataatattt 2400

tcactagata tattattcta aggtaaaaga tttttccttc agcattttaa atatatcaag 2460

ccattctctc cttgcctgta aggtaaggtt tctactgtga ggactgctgc cagatgtatt 2520

ggagccccat tgtacgttat ttgtttcttt tctcttgctt gttttaggat tctttcttta 2580

tccttgatct ttgggagttt aattatttaa atgccttgag gtagtctctt ttgggttgaa 2640

tctgcttaat gttctataac cttcttgtac ttgaatattg atatgtttct ctaggtttga 2700

gaagttttct gttattagcc ctttgaataa actttccacc cctctctctt tctctatgtc 2760

ctctttagac caataactct tagatttgcc cttttgaagc tattttctag atcctgtagg 2820

catgcttcat tctttttgat tctttttttct tttgtctcct ctgactgtat attttcaaat 2880

agcttgtctt caagctcact aattcttctg cttgatcaat tctgctatga aaagattctg 2940

atgcattctt caatatgcca attgcatttt tagctccaga atttctgttt gattcttttt 3000

aaaatttta aaaattctac tttaagttct gggatacatg tgcagaacat acaggtttgt 3060

tacataggta tacatgtgcc atggtagttt gctgcacctt caacccgtca tctaggtttt 3120

aagccccaca tgcatttggt atttgtccta acgctctccc tccccttgac tccaacccct 3180

tgacaggtcc tggtgtataa tgttcccctc cctgtatcca tgtgttctca ttgttcaact 3240

gccacttatg agtgagaaca tggggtgttt gattttctgt tcctgtgttt gtttgctgag 3300

aatgatggct tacagcttca tccatgtccc tgcaaaggac atgaactcat ttttttatg 3360

gctgcatagt attccattgt gtatatgtgc cacattttcc ttatccagtc taccattgat 3420

gggcattcgg gttccatgac tttgctattg taaatagtgc tgccataaac atgtgtgcat 3480

gtgtctttat agtagaatga attatgatcc tttgggtaca tacccagtaa tgggattgct 3540

gggtcaaatg gtatttctgg ttctagatcc ttaaggaatc accacactgt cttccacaat 3600

ggttgaacta atttacactc ccaccaacaa tgtaaaagca ttcctatttc tccacagctt 3660

tgccagcatc tgttgtttcc tgacttttta atgatcagca ttctaacggt gatgagatac 3720

caatgagatg gtatcttatt gtggttttga tttgcgtttc tctaatgatc agtgatgatg 3780

agctttttt catatgtttg ttggccgcat aaatgtcttc ttttggggag tatcttttca 3840

tatccttcat ccacttttg atggagtttc tgtttgattc ttttaaagta ttttaatctc 3900

tttgttaaat ttatctgata gaattctgaa tttctcctat gtgttatctt taatttcttt 3960

gagatttctc aaagcagcta ttttgaattc tctgtctgaa tggtcctatg tcttgtttct 4020

ccaggattgg tccatggtgc cttacttagt tcatttggtg aagtcatgtt ttcctggatt 4080

atcttgatac ttgtaaatgt tctttggtgt taggatttat tgtaggcttc actgtctgtg 4140

ttttttgtt cctgtcctcc ttgggatgga ttttcagata tttgaaaaga ccggagtatt 4200

ttgatctatg ctgtatctgc tttagagggt accacaatcc cagtaatgct atggttcttg 4260

cagtttctag atgtactgct ttgatggtct tggacaagat ccaggataat tctctggatt 4320

accaggcaga tactcttatt ttctttcctt acttctccca aacagagtcc ctctgtcagt 4380

tctgagacac ctgaagctag gagtggagtg aaaccagcac ccctgaggac accaccacta 4440

tgactgtgct cagccagact tgaagccagc acaacactgg gtcttccctg ctgtaaccac 4500

tccctggcca ctgcctatgt ttgctcaagg ccttggggct ctacaataaa caggtggaaa 4560

agccatccag gtctgtgccc ttcccttcag ggtggcaagt tcccccaagc cccaggtggg 4620

tccagagatg ttgtctagga gtcagggact agagtaaaaa acctttgaag tctacctggc 4680

attctattgc attaaaattg agctgggggg actcggggga aagtgtgaga ggggagtagg 4740

ggataaaaga ctacacattg ggtacggcgt acaccgcttg ggtgatgggc accaaaatct 4800

cagaaatcac cactaagaac ttatctgtgt aaccaaacac cacctgttcc ccaaaaacct 4860

attgaaataa taataataat aaataataat aaaatgaata aacaaaaaca ctgagctggc 4920

actcaaacca caaaacacag tctttcccac tctttcctcc cctgtccaaa ggcagaggag 4980

cctcactcca cagcccacaa gaagtactgc tggattatca caggtattca tttaaggcag 5040

aaaggctatt aagtcagctg gtggtgactg ctgcctggcc tgggactcac tctttggggc 5100

agtgggcttc cctgtggccc aggaaaggtc tagaaatgct gttgaagagt caactcttgg 5160

aatcaagggc ccccaagagc ttgcttggtg ctttacctcc ctgtggctga gccagtacct 5220

gaaaccagct agtctcagag gctcacccaa ggcccttgat gtagtatctg ggtatcactg 5280

ctggttattc agagccaaag ggcttttcag ctagcaggtg atgaacgctg ccatgactgg 5340

gtctttccct tcaaagcagt gggttccctt ctggcccagg gtgtttctag gaatgtcacc 5400

tggaagctag ggcctggaac agggacctca ttattctgac tggtgccata tctgttgtgg 5460

ctgagctggt atccaagatg caaggcagag tcctcctcaa ctctttcctc tcctcttctc 5520

aagcagcagg aaggggtctc ttttagagtt gtgagttgtg cagcctggga ttggggaggg 5580

gtgatgccag cactcccttg gctgccccag ctggtgtctc agtatatttt gcacccctca 5640

gtccactgtc tctggcccta gttcagtact aggacttgtc taagaattgc agttcttttg 5700

gcctaaactg cctttcaggt ttagtcagag atccagagca cttcagccct cagtggtgag 5760

gtttgtggga actgaaattc tgactgctgg aattagtgat tccccctttgg ctgggactgg 5820

tttgaatgct ccctttatgt gtgggcatca gctgaacttt gtctggcttt ccttttgct 5880

gtaacaggac aacactgagt ttaatgcctc accattgatg tgttctccct cacccagtgc 5940

acgaaaatgc tctttgcacc acaccacagc tgccagggtg tgatggaggg gtggcttcag 6000

tgcttcaaga ctccttctgc aacctttca gtgccttttt cagcaacaca aagttaaaag 6060

caggtactgc aagtgctcac ttgagttttg gttcttgtga aggagctttg cttgcacaga 6120

tagttgttaa attggtgtcc ttgttgggga aacaatcagt ggagccttct attccaccat 6180

cttgctccac ctcccatagt actatacatc tcttcttttg gctagttctg tttggatatt 6240

tttgctataa taaaactgta gttgtaagta tagtgctttc cagagttctt taatttttt 6300

tagtgaatta tcaagcttga agggttagtg gggattccta aatatggtag ccagctgttt 6360

agaagtatag gtagcttacg taaccttgaa cttgcagctg atgtctgaag taaggacagt 6420

gttatggagg accatgtcct taacttttga agtttggctc aactctagta gttgttgtca 6480

aaagttgatg taacatgcct agtaatttta ggaatgctgg atattgtaaa ggctatattc 6540

ttacttgtct ggatttaatt gacttccttt aaacagtgtt ggactgtgtt aggttacttg 6600

tgagtcatct tgatcctttg ggggattgat tttatgtttt gttaagaaga tagcttttat 6660

tctacctaat tccaatactc tgtagatcat ttctactact aaaccatggc cttctgggat 6720

ctcccagcta gctgtttcct ggagattata aatgactcta acacatcttt catatgcaaa 6780

ccaactaatt cagggctcat acgttcccca accacttcct ttatcaggac tctacaccct 6840

gggccactat tctcctgccc taatcagcca ggtccaggta acagaaaagt aaagacagcc 6900

gctgtacccc agagcctgct aaaagtattc aaacgagcta atcctaagcc tgattacctt 6960

gtcatgccca ctctttcctg cagaaactac agtaaaggct cttgcccacc ttgacccctc 7020

actccagctg cctcctaaca ctggtgcttc tccatgtggt cttgggtggt gtgctgtgtc 7080

ttctgtttgt agggatctgt cgatataaac cttttccttc acgatagtca tttttgtgtc 7140

tgcatatgtt accacattga ttaaaaagag taagttctgt atgattccac ttacccgaaa 7200

ttcaaaagca gacaaaatta acttatggtg ttagaagtca gggtagtggt gtttttttt 7260

tttgcttttt ttttggtttt ttttttgctt ttttttttgtt ttttttttt ttcctggaag 7320

gaggatgtaa ggaggcagga gcacagatcc tgatatgctg ataatctgta tcttgaccta 7380

ggtgcagctt gcaagagggt gttcagtttg tgcaaatcaa ccaagctgta tatttataat 7440

tgggcacttt cttcttgcat gtaatacaga ccagttgcat tattggttcc aattttctac 7500

ctcccactat atccctgccc tttaccatgt aactttacaa atagtctctc actttggctc 7560

tagaatccac catatgactt gatttggcca atacaataaa taggaagtaa gggtgtgctt 7620

gttcttggcc tgagcctgaa gaggccttgt gtgtttcttc tactctcgta cttttgttat 7680

taacattata tagacatggt ggagctagct cactcatccc aggatgagag cctcagctaa 7740

gtttctccat ccaaacacag cctggagctg ggctctaact tgttacacag atgaatgagt 7800

gaatattgtt aagataagtc aagcccagcc cagatttctg acccacagcc aacccacaga 7860

tgcataagct gaagatgact ggttttatca agctaattgt tataatagtg gagaaaagat 7920

catgaggaca aaaagtgggc agagtcggaa gaaaagagag gaagaaattg agacagaaga 7980

catttcattt aaaaaaatat tccattgagc tgggtttgaa atagtgcact gcctgttctc 8040

ctaatgctgt atggtatcat gaaatctatt gtttactgag tctatgagcc agcttcctag 8100

ggaggctatg gcaattgagg acagggaaga ggtaacactc aggaacatag aaggagaatt 8160

tgggtccaag tgggtggagg gaaaaataac tgggtttagt tttgggtagg gctggttttg 8220

aggtctctga aggacatgta agtggagttt tccagcaggg agaaaacgca gagctaaagc 8280

tcatatcttt gctggcaatc tagatttggg catcttcaac aagcaggttg tagctgagga 8340

agctgggact ggacttgtac tctaaagcca gtgcaaaaaa agcttgaaac ggctatgatg 8400

gctaagacct ggcttttcca tgaaaaatgc ttcggtcagt atgagtgatt ccaaagtggt 8460

gatcaattaa aaactgaagt atgattagca ttaattataa cccaatggga atatgataaa 8520

cgactcttgg tcagcaagca gagggtgccc tgtagtgcta aagcatcacc atataccatg 8580

tgtgccaaga atcaggagac accccaaacg ggagcagatg aggggttgtg tctgtcattg 8640

gaccagctgg cctgatccag cagaagtgga tggagataca ctgaatgggg ctcctgggag 8700

gcgtgagttg aaggggaagg aagagaagag acctccaaag taagggaaga gtgaaaaatg 8760

agaaggactg gggtggagcc ccaagtaggg accagaggag aaaacaggga taaagtaatc 8820

aagggagatg ggacaggaag atgaaagaat gaggtaaaca gcaggtggga agaggaggtc 8880

aacctaaagg agaaagccgg gtcgaagaaa gaaggaagag aagaaaagaa gggttgggaa 8940

acagaggagg aggcagccaa gaaagcctgg aagctgaatc atagaacgga agaggtagaa 9000

gacggagggg ctggaggata acataaaggt gggaaacgga agagagaaag aaccgcgtct 9060

gcgtgtatga cggctagaca ggagttcaga gaacagcggg gtcgccaggc caccacctga 9120

tgggccacgg ctcattggct ctaggagctg ggaaagggca tcccaggaaa gaagccctag 9180

actttagcct gagtctgggc cactctaggg gaccgggagt ggggtggcgg gagaggacgc 9240

gcagaatctc gacttctggc cccaatctgt gcatgatcac ccgagctcag cggacgctcc 9300

tctctgaccc aggcaggcgg ctcagggacg cgtgcgggga tgcagagaga aaccgctgag 9360

gaattagggc cgggagagac tggtacctgc cgggggcgtg tggtggggca gagctggcac 9420

tgatgctgag agtggctaag gagcgcggcg ccccagagca gaagggctgg cagacgctca 9480

gagagccagg atggttcagg gtccaaggaa ggtcctatgt tgggtgggag ctgtgaggga 9540

gtgaaagtgc atgaggaacc ggaggagatg gaaagacctt ggcttgggtg ttcgagggtg 9600

ggactgcgtg gtgaccgacg gcacagaggg tgtgtgttgg ggcggaagaa ccaccccagc 9660

tgaatcgtcc ccgtggggtt ttcttcccgt gtcttagttc cagaagtatg cgcatcagac 9720

gctaatagtt gaggaacaag tcatggaagg acagcctaag cgggaggtga atgtaaagcc 9780

gtggagaggg cgggcgaact aagaaggcct tcgttctcct ccggccaccg cggctgcatc 9840

cttgagaaag gggtattgct gcgaaccgcg ccagggctgg acgcggcgag gtgggaggca 9900

ggatggaggg gcgggagcca aggccgaggg ggcggacacg ggtggcgtct ggcgctccat 9960

aaaggggttg cgggggccgc gctctcttct gggagggcag cggccaccgg cgaggaacac 10020

ggcgcgatgc aggttcagtg ccagcagagc ccagtgctgg caggcagcgc cactttggtc 10080

gcccttgggg cactggcctt gtacgtcgcg aagccttccg gctacgggaa gcacacggag 10140

agcctgaagc cggcggctac ccgcctgcca gcccgcgccg cctggttcct gcaggagctg 10200

ccttccttcg cggtgcccgc ggggatcctc gcccggcagc ccctctccct cttcgggcca 10260

cctgggacgg tacttctggg cctcttctgc ctacattact tccacaggta gcgtttttcc 10320

cttgcgggcg cccagtgcag cgcactgccc tgctcccggc gtccaggagc gcagcgtaga 10380

gcgcgcaccg aggaacgcca aggaggcagc gtggggcgct gtgaggaacg cggaggccag 10440

cctgcctggc gcacctggcg ggggccgggg ccggggcttg gacgctagag agttgacaag 10500

cggctgcggc acagacgccg ccttcactcc cccaggacct catccgctct cagcagctcc 10560
aaatcctctg gctgctcgag agaaagaggt cctgcgggcg ggaggcgacc tggaaagctc 10620
aggttgggga gacctattgg acaggactgt tccttaactg cgcgcaggcg gcggttacct 10680
gtggcatatc gcgccccgcc ccgcttccct ttcttccttc acctttтcct tgcagggtgg 10740
ggacagatta gttctgggat cttgggagag tcttacgcgt ttggcatctc ccgagggaaa 10800
ctcagctcag aggttctcat tgatttagtc tttgcaggtc taaggaggaa ggtgggtaga 10860
gcccaaatcc agacttcaca gatggggaag agaatatagt gagatcccac tgactcaagc 10920
gagggtcccc gcttcttagg cccctcccaa aagggaccaa gcacaccacc aattcatcta 10980
cctttccaat ttccctggga cttgaaatgt gagtgggtaa cttacagctc aaatgttctt 11040
ctagatttaa aaaatccggg ttcaggagaa ctttgctttc tgctctggga aggaaagaca 11100
ggaaagagac caagggatgt tagggttcag agaaagactg tccagcctca gtaaagtctc 11160
acagggaaag ggaagaacga acacattgtt aaattgccta ccatgcccaa tcgtttagta 11220
tctatggtct cacttaactc tgttgtaacc ttttgagaga tatttattat gtccacttta 11280
caaagaaact gaggctgagt aaggttatgg gactgaaaga agacaataca gctggtgccc 11340
gctaagatgc aaatctgagc ttgtgaatct ctgaggttta agacctttta gccgttttaa 11400
gtaggcagat attctatgca agaagagaac agagcccata aacagagaaa agttatcaaa 11460
cgaaatcaaa accttgaagg ttttgcctta ttttgagtag aagattccta gggtcaaaag 11520
atcaaggaag tttggattag aaattaggat aaagaatgcc tctggcataa tctgtctcgt 11580
aaagagaaag tgatgcctca tttcgagaga agaaggtgtc agagacggat ttcaaactgt 11640
ctttcttaat ttcctcttat cctctgaatc ttctttattg gtcaagattt aatatttatg 11700
caatcttaac tgaattctca ctctttttaa aaggcaaatg ttgtcaagta ataagaacta 11760
aactgtatcc tttcaacaaa tatttactaa aagcctgctg tgaacaagat tctttatttt 11820
acacagattt tattttactc agatttagat ggtttaattt gcacagaaag aaggatgttg 11880
gatacaggag ataagagatt agtttttat ttcactgatt tttgaacaga catttgacag 11940
aaatgtgatt tttgtcaaca attatttta tcttcaaatt aactactgta tgttggcaac 12000
ataagcaata tttttatgag gtcatttcat cttaatgatt agtgttttgt gacaatcata 12060
ttaatgtaat ctttaggctt gtttttgaaa tcaaaaggca ctttgcacaa tacattatga 12120
ccggtgcatt taaaaaaaaa cccaaaggag taattatgca taaaacaaat atctacatat 12180
tgtccttctt cagaggaaat tttaaaatat tagtaaagga cttggagatt cattctgcct 12240
gagggaaaat tgcccactgg aagtacaact cttgagctac ttgttcctga ggcatcggga 12300
tctgatgttt gtctttcctc ttttttgaat tctttctttg aagccactgg agtgtgtgat 12360
ctgttattat ttgagtgctt acagggtgtt acactctgtg tgccaaacac tctgagttaa 12420

taatttactc atcctcatac caacccattt aggtaggcac gcccattttg caggtggaaa 12480
actggagcaa gaaaaggtta aataacttcc ttgcccaagg tcacacaata acgaggaatc 12540
agagttcaaa cccaggcagt agactccaga tctcaggctc ttcaggtatg ataataaact 12600
gttgtatact tgttggataa atgcgacctc attcttgctt tttaaaaact atatttattc 12660
ttaaaattat tatgtaaaaa ttttttaaat tataaaaaca ttttttccta atgaaaaatg 12720
gaaaaatccc aaaagtagaa aatactcata attacatcta agtatattaa atattaatgt 12780
tttagagaat ttctatcaaa tctttttcct tagtagattt tcacacatgc ttgttatgtt 12840
gaatatatgg ttttttagtt ctgtttaatt acctaacatt ttatagtatt ttccaacatt 12900
atcacagatt tcttaatatc tgcttatttc atctactgta aaaataataa tttacctata 12960
tattcattta tagttggaca tttaatttgt cttggggtga ggctaggttc attgaagctg 13020
tgatgtacat tttttgcatc taaattcttt tcaaaggtta gatctatttt cttaggattt 13080
ccagaagtgg ttcaaaggtt atgaacattc tttagggtct tgatataatc atacatatct 13140
gtttcgaggc ttaaggagtc atttggcttg atactgaggg tgcattaagg aacaagcatc 13200
aggctgtctt ggctttatct cgtgctgtgt gttgctaaga cagagaataa gacggagaga 13260
cagggagaaa ggatggctca ggtttggctc agactctttt gcaaaatgtc cattggggac 13320
tgttcaaagc agcaatatgt cccatcaaat agaagttaaa actcattgta cttttctcaa 13380
tacaaggatg gcacacaaga atgtagattc cacagggtca aaggtttttg tctcactttt 13440
atggctgtat ccccattgta tacaaagagc tggtacatag ttggtactca ctagaatttg 13500
ttgaatgcat gaatgaactc tacttacaac aaccgtacag acagaattgt aggagagcta 13560
gcaattactt gggaatcata attgctgaga ttgcatagtt aggtcaattc agataacttt 13620
cctctcttca gaatctattg ttgtggctgt ttggattctt tagccacatg gaaatgactg 13680
ctgcctaagc acattgccta atcccactgc caaaggcatt tgaagtcaag agttatctca 13740
cctctttttt ttttttttt ttttaatgtt tttttttta ttatactcta agttttaggg 13800
tacatgtgca cattgtgcag gttagttaca tatgtataca tgtgccatgc tggtgcgctg 13860
cacccactaa cgtgtcatct agcattaggt atatctccca atgctataag aaaaaccaac 13920
acagagacca ccacagttcc cagagtgtga tattcccctt cctgtgtcca tgtgatctca 13980
ttgttcaatt cccacctatg agtgagaata tgcggtgttt ggtttttttgt tcttgcgata 14040
gtttactgag aatgatggtt tccaatttca tccatgtccc tacaaaggac atgaactcat 14100
catttttat ggctgcatag tattccatgg tgtatatgtg ccacattttc ttaatccagt 14160
ctatcattgt tggacatttg ggttggttcc aagtctttgc tattgtgaat agtgccacaa 14220
taaacatatg tgtgcatgtg tctttatagc agcatgattt atagtccttt gggtatatac 14280
ccagtattgg gatggctggg tcaaatggta tttctagttc tagatccctg aggaatcgcc 14340

acactgactt ccacaatggt tgaactagtt tacagtccca ccaacagtgt aaaagtgttc 14400

ctatttctcc acatcctctc cagcacctgt tatttcctga ctttttaatg attgccattc 14460

taactggtgt gagatgatat ctcatagtgg ttttgatttg catttctctg atggccagtg 14520

atgatgagca tttcttcatg tgtttttttgg ctgcataaat gtcttctttt gagaagtgtc 14580

tgttcatgtc cttcgcccac tttttgatgg ggttgtttgt ttttttcttg taaatttgtt 14640

tgagttcatt gtagattctg gatattagcc ctttgtcaga tgagtaggtt gcgaaaattt 14700

tctcccattt tgtaggttgc ctgttcactc tgatggtagt ttcttttgct gtgcagaagc 14760

tctttagttt aattagatcc catttgtcaa ttttggcttt tgttgccatt gcttttcgtg 14820

ttttggacat gaagtccttg cccacgccta tgtcctgaat ggtaatgcct aggttttctt 14880

ctagggtttt tatggtttta ggtctaacgt ttaaatcttt aatccatcca tctcacctct 14940

tgttgactgt gattacagct gtggaatgac cccttgtcta aactctctga ttggtcttca 15000

ctttcccaag aagtcttggt gttccataca gtggtcagtc acatcactta tgcatgtggt 15060

ggctgatgtc tttttcaaga ctttgatggg accttgataa ctgaatgaac aagacaaaga 15120

aacatttttt tttccagaga agaagtgact acattgtgaa aaggttttgg gcaatgtaat 15180

ttccatgata tacatctaga agcagagtat aatgcacaca ttagagtctg tttgaattcg 15240

gagagatatt ccttgaggtt tagatgctga aacatttttt tgattagcca aataaaatga 15300

tggcttcaat aaggtgcttt ttgctttatt agtcagttca ttccccagcg gaatttctcc 15360

tcatccttca agattcaggt caggcatcct ttcctccaag aagccttgtc tgagtctttt 15420

cttttctcta aatccagttg tgatgctgtt ctttgggctt tcataatagg cagtgtggct 15480

ttcgatgagg catttcacac actggatcat aattatctgt tctaaggaaa cgtagttctc 15540

atctgcccag cctcttcatt ttacagaagc aaagcacaaa aggttgggtc agttaggggg 15600

aaatcaaaga gttggaactt gagtcttctc atgagcccct gccaatgctt ctcttatttc 15660

acgagaggtg cagatgtctc aactattcag aagtaatcag accttgctaa ggaaactact 15720

catctgctga gaatcagaat gagaattaat ggctactttg gaaacaatag acaaatctct 15780

cctcttagag attaagaaaa aaaaagccca agcaagaaaa gcaacattcc tgtgatcact 15840

taatcatgtg ttaaggatgt tcctgaatca taatttaaat aaattaagat taattgaagg 15900

atttttttag aatgagagtc agcaaacttt ttctgtaaaa agccaggtca tgatctctat 15960

tgcagcaact cacccctact gttatagcgg gaaagcagct acagacatta tgtaaacaga 16020

tgaatgtggt tgtattccaa taaagcttta tttacaaaaa caagcagtgg gccatatttg 16080

gcctatgggc catagtttac caatcccttc taaagaaaac tatgaatggc gtggctttac 16140

attcagtgcc ctggtaattc tataataaaa tttggttaaa ttctatagca aagcagcggg 16200

catatcttag aaaatttctg ctacatgtaa gtggggactt ggcagtaaat attgttttct 16260

gagaattctt gggttctaag tttttatttg aacttttatg ggaaaatagt aggagtcttg 16320
gagttttcat tctaaatgga atgacatcat aagcacatct gaaaaatata tagctatgtt 16380
tgccaaaaat ataaaccagc tttggagatc gtgaccactt cacttttacc acactgaaga 16440
aaggaccaac tttttgtcca tttaaaatct aatttaatgt cacttaaaaa gaacaaacaa 16500
aataaagaat tacgatggga attcaaggat tcagactggc aaagtgacat gtaccaagtt 16560
acatggcaag aaagggcaga gtggagcttg aagcctggtc tcctgatctt tatcagagtt 16620
ctataggctc agaactatgc taggtctcat gggagtcata ggagtacaat acctagtgct 16680
tgccctctag gaagaaggca ggaaagaacc ttcattgtgt gcttctcact ctttctggtg 16740
tgaaacttgg gtggcagcaa cgtcagtctg acaatatcag gcaggtggga aaatgtaaac 16800
tgaggggggaa agaagcctgg ttagcacggg ccccccgccag gccactgaac attcatctga 16860
gagggcccta gtgcctgtct atgtttgatt gtgcatggga caggggggcag atagataggt 16920
ggataggtgt tgaggggggcc tcaaaatggc acccttcttc tccattcaag ttcagaacta 16980
actgagagat ccaggaatta ggtaactaga gacatattac caccttttat tactggtaaa 17040
gctggtttgg gggaatgtgg cttagatttt tggattatat gggccttata acacagtacc 17100
tcagaaataa ttagctatga tcatggctgg gcaaccacag gcctctcaca gtggtacctg 17160
ttctgaaaag acagcagaag ggctgagctg tacgcatcct ttggcaggtc ctgctcccag 17220
attgacccat caggtaattc acatttcctt gcctgaggag gaatgggtga gggacagtgg 17280
aagggcttgc agtgatgctc taatgaaggg ccctcagcca gctgtagggg gagcataaat 17340
atttttgtt actagatgga atacaaacgt tgtctactta ttgaattttg ccacagcctg 17400
gcaacttgtt tctgcaactt ggggtacttc ccgttctgct gttgactccc tgccatgtat 17460
ggcaatgggg acatcaaagt ctggactcaa gttgttttaa aagtttctgt gctcaaccca 17520
ggagccttta acgagactca gctcaacata ggagctctaa attttaaaaa cccctgaact 17580
agggccaaca gtgcaatttg tcttccattt ggttatagaa gggagagaag ggaaaccaat 17640
atttattgcg ctctgggtgt tccaggcatt atattatgtt ctttgcattg gctatctcat 17700
tttgtccttg aggcaatccc tgttattagt gctattttac aagtgattgc agtgcagagc 17760
attgatggag tgagtgggag tgaagatggg agacttgacc tggtccttga agaatggcct 17820
gttcccagat ttctgggtgg ggacatgatg tctgttggga aaaggggccc atttggtgat 17880
ctgtgactta aatttgcctt atactttgta tactcagtct tggagtatct ctctactttt 17940
agattccaaa catcttctgt aactatgcca tattatccag tcctactacc caagtcttaa 18000
attaggctct gggcctcttt caatttcttt tttttaatat ttgctccata ttgttaaggc 18060
tgatcctaga agttactgtg aagaaaacag ggtaatttgg ttttgatatt ttttctttct 18120
aaccacgaaa catcccaaga tctttttttca tgtatagact ctggttctct cttgcctctc 18180

tgcctgccct cttgtatcag cagtacatga tcttacttct atcttttaaa acttaactct 18240

gtgtctcatg ctgtcagtca atgcccttta cttgccaaaa gttactcatg tgataaacaa 18300

atctaagttc tagtgtattg ggttgtttgt tttcttatta ttgagtttta aaagttgttt 18360

atgtattctg gatagaagta ttttgccagg tataaactta gcaaatattt tctctcagtt 18420

tgtgacttgt ctcttttatt ctcttaactg tcttttgttt taaaaaaatt atttttaggt 18480

tcaagttaac atatgcagtt ctgttataca ggtaaactac atgtctcagg ggtttggtgt 18540

acagattatt tcatcacccc agtaataagc atactacccg ataggtattt tttcaatcat 18600

caccctcctt ccatcctcca ccctcaagta gaccccagtg ctgttgttct cttagtatcc 18660

atatgtactt ggtgtttagc tcccatttat aagtgaggat atgcagttgg ttttcagttt 18720

ctatgttagt tagctgagga taatggcctg caaaggacat gatctcatta tttttcatgg 18780

ctgcataata ttccatggtg tatatatgcc acattttctt tatccagtcc accattgatg 18840

gatatttagg ttgagttcat gtcttgactg ttgtgaatac gtgctgcaat gagcatgcac 18900

atgcatgtgt ctttatggta gaacaatata tattcctttg gggatatacc caataatggg 18960

attgctgagt tcaatggtga ttctgtttta aattatttga gaaattcctc ctagcagtgt 19020

ataggcgttc ccttttctcc ataaccttgc cagcatttat tatttttgac tttttaatag 19080

tagctattct gattgatgtg agatgatatt ttatggtggt tttgatttgc atttctctaa 19140

tgattagtga tgccgagcat tttttcatat ccttgttggc cacatatatc ttgttttgaa 19200

aagtatctgt tgatgtcctt tgcccacttt taattgaatt gtttggtttt tgcttgtaaa 19260

ttagtttaaa ttccttatag atgctggata ttagaccttt gtcagatgca cagtttgcag 19320

atatttttc ccattctgta agttgcatgt ttactctctt gatagttttt tttcctgtgc 19380

agaagctctt tagtttaatt aggtcctatt tgtcaatttt tggttacgtt gcaattgctt 19440

ttggtgtctt tgtcatgagg tctttgccag atcctatgtc cagaatggca ttttctaggt 19500

tttcttctag ggtgtttatg gttttaggtt ttgcatttaa gtctttaatt catcttgagt 19560

tgatttttgt atgtggtgta aggtagtggt ccagttccaa ttttctgcat atggctagtc 19620

agttatccca gctccatttt gaatagggag tcctttccct gttacttgct tttgtcaact 19680

gtattaaata tcagatggtt gtaggtatgc agcattgttt ctgggcactc tatcctgttc 19740

cattggtcta tatgtctgtt tttgtaccag tgccacgctg ttttggttac tgtagccttg 19800

tagtgtagtt tgaagtcagg taatgtggtg cctccagctt tgttcttttt tcttaggatt 19860

gcctggttat cccagctctt ttttgattcc atatgaattt taaaatagtt tttttctaat 19920

tctgtgaaga atgtcatcag tagtttgata ggaatagcat ttaatctgta aatcgctttg 19980

gcagtatggc cattttaaca atattgattc tttctatcca tgagcatgga atgtttttct 20040

gtttgtgtca tctctgattt ctttcagcag tgttttgtca ttctcattgt agagatcttt 20100

tacctctctg gttagttgta ttcctaggta ttttattctc tttgctgcaa tcatgaatgg 20160
gattgcattc ttgatttggc tgtcagtttg gatgttgttg gtgtatagga atgctagtaa 20220
tttttgtaca ttgattttgt atcctgaaac tttactgaag ttgtttatca gaccaagaag 20280
cttttgggaa gagactatgg ggtgttccag gtatagaatc acatcatctg caaacaggaa 20340
tagtttaacc tcttctcttc ctatttgtat gccttttatt tctttctctt acctgattgc 20400
tctggccagg atttccagta ctatgttgaa aaggagtggt gagagagggt atccttatct 20460
tgttctagtt ttcaagggga atgcttccag cttttgccta ttcagtatga tgttagctgt 20520
gggtttgtca ttgatggctc ttgttatttt gaattatgtt tctttaatgc ctcatttgtt 20580
gagggttttt aacatgatga ggtgtttagt tgtattgaaa gccttttctg aatctattaa 20640
gataatcatg tagtttttgt ttttagttct gcttatgtaa atcacattta ctgatttgca 20700
tatgttgact caaccttgta tcccagggat aaagcctgct tgatcctggt ggattagctt 20760
tttgatgtcc taccagatta agtttgccag tgttttgtta gggatttttg ccctgatgtt 20820
catcagggat attggcctga agtttttctt ttctgttgtg tctctgtgag gttttggtat 20880
gaggatgatt ctggcctcat agaatgagtt ggggaggagt ccctcttcct caatttttg 20940
gagtagttta agtaggagtg gtaccagctc ttctttacac atctggtgta atttgtctta 21000
actgtctttt gaaaaacaga aatgtttaat tttgatgaag tctaattttt ccatttttct 21060
ttggcttttg atgtgatatc taaaaaattt ttgcctaatc taaggtcaca gtgattttct 21120
cttatatttc cttctacaag atttgtagtt ttaggtttta atttcaggtc tatgacacat 21180
tttgaattaa tttttaaagt aggtttccaa gtttgaatca aagtttttt gttgtgtttt 21240
ttttttttg ttttttgttt tttgcatgtg gacagtcaat tgttttagta ccatttgttg 21300
aaaatactac tttttgtcca atgaactgcc tttgcacctt aactttaaaa ataggagaat 21360
tatatgaaca gatactttgc caaagaaaac gtatgattgg caaacaagaa catgaaagga 21420
tgctcattat tagtgattag ggaaatgcaa attaaaccac aatggggtat cactatgtgt 21480
ctgatagaat ggctcaaata aaaaatactg accataccaa gtgtttgtga ggatgtggaa 21540
gagctggaac tctcatacct ttgatgggaa tttaaatgac aaccactttg gaaaatggtt 21600
tgatagtttc ttaaaaagtg aaacatatac ctatcatata atgtagccat tgcatttctg 21660
gttatttttc taagaaaaat aaaagcatgt gttcatacaa atggtggtag cagcagcctg 21720
actggagtgg ctgcagtgtt agaggcatgg ctggggctgc gcactccaca gagctggcac 21780
ggccaggaac aggcatgagc cccatcccct accaagttgg tggggcagaa ggccagtgct 21840
ccttggcgca gctgcagcca cccagccatg gctctggacc cgggcttccc tgtgctctca 21900
ggggcctggg aagcgcccct gcccctgaag gcttggaagt acctgctccc gctccttggc 21960
ctcttcccac tctaggcacc tgctctgggg tggaacaaag ttgtggctga gccaaggtgc 22020

tgttgctcgg cctggcatgt gcaagctcag ggcggcattg acacaccagc cccctgccgc 22080

cttggccccc tccagacttt gggtgctgat gagcatggga ggaggggcaa gtgggggctg 22140

agggtggctt agtgcaggct tgcaagcacc ccttggcact aacagcctgg gcaccatgga 22200

tggcatgtgg atggtggcag gaggcagaca ggctcctggg tggaaagggg caggtctcgg 22260

gtgaaacccc accttcaagc cagggatggc ctgaagcctg ggtgctgggc tgtcaattct 22320

ggatggagtc agtggcccag agtgacaatt tatggtgctt tttctgaacc tgctcatggt 22380

ggcccatgga ccaatcagca cgcccttcct tctgaggcta taaaaactct ggactcatcc 22440

agacttgggc agacatcagg actaccagct gtgggaagga actgcccact ttgggtctcc 22500

cgagagcctc tctgtcactc actgaagctc ctctctgcct tgctcatcct ccagttgttt 22560

gcgtacctca ttgttcccgg acacgggaca agaaatcagg acctgctgaa tgcggggact 22620

gaaagagctg taacacaaac aggtctgaaa catgcccccc tgcttgtcac attgcaggca 22680

acaagaagga gagaagagct gggacccttc ggggagccca gaactagggg agccctgagc 22740

cagggctatg acaccctctt tggggctttg tggttcctgg catctccaag cttccaggca 22800

ccaccatgtt cccttcatcc agatgtgggt gcccacagtg gaagccactt ggggtacatc 22860

tggtccaacc atagcctcac atggagccgg cacttatgct gtcatctgga gctgcttgcc 22920

ttgcccagca accagtgtgc ctggctgtgc acagtggctg gaccctgcgc tcactcacac 22980

acacacccct catcattctg tgcctggctc acccttggca ggtgtgggat ccaggcctgt 23040

agcatgagcc aagtgcagcc tgccaggctg agtggacaga ttgagctcag tgggcatgag 23100

caatactcag gcagaaggca ctactggcca cagaggtttc cagctggtga agtgacaccc 23160

caaggatctc gtgacacaaa gacttgtata caaatgtttg tagtagcttt atttgtacaa 23220

gccaaaaact aggagtacat gctttatgat tatgtttata taaaattcta tgaaatttaa 23280

actaatctat ggtgacacaa agtacatcag tggtttcctg aggacacaag agggacaaga 23340

aggtagaact acaaagggta tgaagaacct tttgttgtga tggatgtgtt cattattttt 23400

atgtcacatg gcttcatgtg acatgaaata tatctaccaa actgcactgg tagatatata 23460

tatatatata cacacacaca cacacacaca caccaaattg caccctttaa ataggttcag 23520

ttgactgaat agtaatttac ttcaataaaa ataagaaaac taggtaggcc tgtgaaaaaa 23580

ttatatgtat atgtggccct gtgtcactga gaattgttca aagtttctgt gaagttcatc 23640

tggaaatgtt caacaagtgc tgataagctg tttcactttt ttgaggtgtg agtagaggag 23700

ggccaggaat tctactcaag ggaaataatc caaaaggaag aaatcagtct acacaaagtt 23760

atagtgttac tattcacaac tgtgaaacac tggaagttac ctaaatgctc tacaattggg 23820

gattgattgt aatcaatatg attaaattac catatatatt tcaaaaatat tagttgcatg 23880

gactatatct gtgtatggaa ataaatatat ggagccattt agttaaaaag tagcacataa 23940

agagtacact ctgatttaat ccatgttgac atgtacaaat gaaaattgac catgattgga 24000
atataaagtg atgtaaatag ctgataattt aggtttgtat tttttccttt tagtattatt 24060
aaagtattta attatttaac tcctattata ccttatagaa gaaataatac tgtattacaa 24120
aattttaaga tgtattttac aaactgacca tgcaattaaa tctcagcaga gatatgacac 24180
cccataagta gttactgttc tgagggattt taaaagtcac acttcgtgtg tgagatctcc 24240
cccactgagc tgctatgaca caacccactt atgaaattgt catctttcta tttctccttt 24300
gtatcaagat gttgatgatc ccttaacatg caatcatgtt acctggcaaa gtagcacttg 24360
gcaaagtcca aactattatc cttttaatat tttgaatctg agaggatctc atctctttca 24420
tccttaatca tggtaattta tattttccac tttttttcca gatctttttg actagagctt 24480
tagaaattgt attgatcatc tcagaactag atttttattt cattgagttt cactattgat 24540
tttgttttac atttaattgt tttctgtttt gatctttatt atgtttttttc ttatgcttac 24600
tttgaatttt atttgctctc ctttttctat ttttattaag gtggaagcca aggttataaa 24660
tggagacttt ctctttcttc taatatgagc atttattgct ttgaatttca tcctacatat 24720
tgttttgtgg cacctcacaa attccgacat gttgttacca ttttaattta tttcatgtat 24780
tttaatttct cctttgattt attctcatat ctatgggtta tttagaaggg tgttatttag 24840
tttccaaatg tttaggaatt ttccagacat gttctgtatt catttctaat ttaattccac 24900
tgtggataga gagcatactt tgtatgacat acatcctttt aaacttactg aatttaaaac 24960
ttgttttatg gcccagaatt gggtctatca atcgtaataa ttgttctgtg taaacatgaa 25020
aagaatgtgt atactgccaa gaagaggagt gttctaaaat tgtccatagg ttattttgat 25080
tgttagtgtg cttcaaattt ctatatcctg atgattttct ctctacctat tctaccagtt 25140
attgagagaa gagtattgag atatctgatc aaaattgtag acttgctttt ttttcttaca 25200
gctctatcag tttttgcttc atgtattttg aaggtctatt attacatgca tagagacaga 25260
actggtatgt cctcttgatg aattgatgct tttatcgtga tgaaacaatc ttctttattc 25320
ttggtaatat cttgctttga aatctacttt tgtcttatat taacttagcc actacagatt 25380
tctttttact agggttaaca tggtatatgt atctaccatg tttattccaa cattttactt 25440
ttaatctgtt tctgtcttta gatttaatgt gtgtgtctca aaggtggcat actgttcaat 25500
ttttctttcc ccctgcccct gccattctga caatctctga tttttaactg ggatattaga 25560
atgtttatat ttaatgagat tatttataca gtttgaatta tgtctatcat cttgctattt 25620
gtttccattt gtgtctctgt tatttgttcc tatttcctat ttatattcca tcttttggat 25680
ttagtattat tttatttcaa tttatattgt cagtttattc attataactc ttttgttaat 25740
ttgcttaaag gtttattgca tgtatcttaa atttatcagt cttccttaag gtgatattat 25800
accacttcaa gtatggtata aaaatctgaa ataatgtact tccatttctt ctctcttgcc 25860

cttatgttat tgttgttgtt ttacttacat atgtgctata aaagcctcaa cttattacta 25920

ttatttttgt ttaaatcgtc aattatcttt taaacagttt taaataagat aataaaaaag 25980

ttatatattt gcttatgtgg ttgccatatt tgatgctttt cattttgag ggttgattta 26040

tatttctatg tggtatcatt ttttcctttt acctgaaatc agaatttata tttctgaaag 26100

tgtttttatt tcttgttttc gaagatagaa aattctagga tatagcaatc cagattgaca 26160

gctgctttct ttcattactt taaagatgtt tcactgtcgt cttgtttgca ttatttccaa 26220

caagaaatct gttcttgccc ttatccttgt cctctgtact taacgtatct tcttatcttt 26280

gcctactttt aatattttca tgttatcact ggatttgaga tgttgggtta ctatattcct 26340

tggtgtattt atatttctta ttctgggctt ccttaaactt gaatccatga gcttgagtct 26400

ttcatcaaaa ttggacgatt ttcatacact attcttcatt ccctccctac ttctcctttc 26460

ttttgctgag gaaaatatct atgagaccta catgtatatt aaactgtcct acaactcact 26520

gatgctcttt tcatttttgt ggattctttt ttttttctgt gtgcttcttt tgggtaattt 26580

ctattgctat tcttcaagtt cataatcttt tcttctacaa tgtcttatct gttgctaatc 26640

ccatctctgg tatttttatc tcagggattg tagtttccat ctctagaatt ttggatttcg 26700

gtctttttt ctctcttcca tgtccctact taattttgtg aacacatgga atgcagttat 26760

aacagctgtt ttaatatcat tgctaaccta atatctgtgt catttcggtg tcagttttga 26820

ctgattaatt atttttccta taataagcag tgttttcctc ccttttgca tgcctggtaa 26880

tctttgattg gagggtcaga aaattgtacc tcattgggtg ttggatattt ttgtgtttct 26940

ataaatattc ttgagctttg ttctgggatg aagttaagtt acttggaaac aatttgatca 27000

tttcaggctt tgatctgatt tgttcagtgg ttccagaaga gtgttaatgc tagggctaat 27060

taataatttc ctctgaggta aagccttttt gagtattcta cccaatgtct tatatgagct 27120

tttctatctg gcttatgggt acaggctcta tttgtggcca tgtgtgatca ctggatactg 27180

ttccctttaa ttcttttggg tgattctttc ctcacacaaa tgcatgaatt aacactctgc 27240

taatacttga ggaaaattct ctgcaggtct ccgtgtgtct ctgtcctttt cagcactctg 27300

tcttgaaaat tctagatgtc ttgatttctt gaaatctcaa ttttgttttc tcaactcagg 27360

aagtctttta gcttctccct gggatcccct tccctgtacc tcagcctgga agttttctca 27420

aaccaggaag ctgggtcagt tatgaggtgg tgtgagtcat ttttttcttg ccactcactg 27480

tttttcattg cctaatatcc agtgttttgt aaataattat ttcatataac ttacctttt 27540

tttttctagc ctggaggata aatccaattc ctgttattcc tccttgactg gaagcagaag 27600

tgtctccaat gggttttagt atttatcttt gctaattgga taatctgcaa tactggttga 27660

tttgttggtt ttagtgacct ctacttgtac tcaatgtcat gtttttttcc ccaaactttc 27720

catcttcagg cttgacgtgt aatgctttgg gacgtatttt acttagaaga ctaagtggga 27780

tagcagaatg atgacttcct ttacatgagt cctgtggctc catgtagctg cagctgggaa 27840

ggtggctgta ggactataga gtaggagata aagagtggga gataccaaca gatggttatg 27900

aatgattggt ttgaaacttt cacatggaaa attatgttgc agaaacctca gattgtgctt 27960

ttgttctttt tttgtttggt ccaaatgaac aatggaatgg aggtagatgt aggagggaga 28020

tatgctgagg tagatcaatc tttgaatgtt gcctttgatc agggctactg aatccctgga 28080

catttattta tttgttttaa aaatttaatt caggggggtac atgtgcaggt ttgttacatg 28140

ggtatattgt gtgatgctga ggtttgagct tctaatgatc ccatcacgca agtggtgaac 28200

atagtaccca ataggtagtt tttcaaccct tgcccctctc cctccttttc ccttttggaa 28260

tccctggtgt gtattgttcc catctttgta tcaggacaat atttaaatgt aggtggaaac 28320

tttttaaaag ttctcaaatt tatggcaata tctaggcctc attgctgcaa aactgtacag 28380

agctgtttgc ttccaaataa catcagaaga cttgggattg ttaatgggta cattaatatg 28440

attagattga atgaataagt tctagtattt gatacagact gactacagtc aataataatt 28500

tattactcat ttaaagataa ctaaaatagt ataattggat tgtttgtaac agtaaggatc 28560

aatatttgag gtggtggata ccccatttta ccctaatgtg attattacac attgcatcct 28620

tgtatcaaaa tatctcatgt accacataaa catatacact atatacccac aaatattaaa 28680

cataaaaatt ttttaaaaag gaaaaaaaag acctgtaaac ctgggctgca ctaagaagct 28740

aaacaactga acttagaaaa ccacaatttt ctttttgcaa acattgagaa ataaaggaga 28800

caaaattata gctcagagaa atggcatgta tttatccaac agtgaaagtg cctgttatgt 28860

ccttagctgc tcttcatagg cttgctgagc tttttacttc aagctgaaaa ccatcccatg 28920

tcaatatttg tattttcttg attttgtaat aatcagttag catgagtggc tgagcaactg 28980

ttgtttcatg atgccaaaat ccacctcaag ttgatcaatt tatagaaaac ggtaaactag 29040

ttattcaaat aagttgattt agttactcag gccatgaagt tgatctgatt ctctttgatt 29100

ttgatcttct ggggtattaa aaatttttt aaaatggagc cagtggtcag tagcatgcct 29160

atgggaggtt tcactccaat gatcattatt ctttctatca ttctggggaa tcctcaaagt 29220

tttttaaaac cttggtaatt cattagatgt ttggattgaa catctatttt aatgtagagg 29280

caggaagaaa gatactgagt ggacagttcc aaggtctccc agtattacca ggacatgcca 29340

taaatactta aaaacataag cagggaactt aaaggttttc tgctgtattt tagatattca 29400

caagctaatc atctcaaaga ttttgcatga tttaaatgga tctgccagat taggaccatt 29460

agatagttaa aaccagataa catttgcatg gggttgacaa tgggatgtgg ctgccctgtc 29520

ttccagcatg gcagagtaag atgggaagaa gtcttgagtc attgctcttt ggggaaaata 29580

tcattatatg tctaggaggc cttaatattt gtcttactag agaaagtaat taggttaata 29640

ttgctgtgct aatagagtct tggagcctga aaactgggct aatccacact gtaaatactg 29700

gaggccgtgt gtttccccag ttagggcaca cttggagagg agtcaggtgt gctcttttac 29760
aaatctcatt gcattattat tgagctcttg gaaaggtgct gagtcttcat tttagaaaaa 29820
gggattagat gtggagggaa tcactttgct ttccccaggg aggcatttct ctattgcttt 29880
tctagggttg ggataggtat atagaaggtt tgattctaga atttataaaa tgatattctg 29940
ggaactttga gcaatatttt agggagggca cccatccaaa aaactagatg agttgctgcc 30000
tttctctgca acagccctta ggagactagc ttctgatctt cttcctaaac ttggtatcca 30060
gtttatttg cttgtcttcc tgcaggccat tcttgtggag acaccgagta acaaagtctt 30120
gaagtaatgt gtgacaagct ctgtagggct ataggattat agagcagcta ctcagagggc 30180
aagggtatga agaaaaagag caggtgcata aaaggaacag ggaaagggga gtaaaaggaa 30240
atggggaaag aggtttaaag gagatacaac agtaaaaaga agaaaagctg ggaaaggaga 30300
aaggaagcgc agcaaaaaag gtggaaaaag aagagagagt gctgatgcag gtttttcagg 30360
ggcctatatt gggcaaagca ttgaacaagt tacacccaaa ggccaggagc ctgaaatcag 30420
gtgccggttc tcaaataaca agggcttatt aagaatcagt gctattgcct aggatagtta 30480
aacagaaata caaaaagtgc tggagaagtt cagggaactg tgagatatag agggaaaatc 30540
aggggaagat ggacaggaga tgggagctct agacaccctt agacatcttg gtttcaggtt 30600
cattggtcag aactctctcc ccatccccac agtctatcta gatgcttaca tcaaaggcaa 30660
tgcttgcttg acagatttct aaatagcagt agcaacaaga tggaaagaag aatggaatgt 30720
cccattagag gatatagggc caggacttca gaaagagttc atatatatta atcacatgtc 30780
ttagaatatc ctggagcacc tgtcctctca cctacctaaa atacttgatt cccaatggtc 30840
aatgactttt taaaaaaagg gggggggggg gattggtatg tacatagata ttgtgggaac 30900
gtacaatttt ttaaaaagtg atgataaagt tctataggta ccttcacaaa ccactctgtt 30960
ctacttaaat cttaacagtt cctggaggaa actttgagat tactcttcag agcttacttt 31020
ggtggttggg gtgtgttgta tggctttgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg 31080
tgtgtgtgtg ggtttgttta cttttactta tgggcactga tgtattggtt actagaaagt 31140
tcatagataa atttttgtcc tattcagtag acaaacatac ctgacttgtt gacatagagt 31200
ctaggtgcta acttcattag tcaattcacc ttactttcat atctttattt tcatttgcct 31260
ccttttttctt taaattttag gccatcttac agcactttat acatctatgt ttatggcctt 31320
aaatcttttc tttttctttt tttaagagca atttgggaag aactaaaata aaattgaaat 31380
acaaatcaac atttttttgtt ttatgcaaat gtatgttaaa atattcaaag aataaagagg 31440
ttttttaaag aatagtaggt tctagcacgg ctcagttaaa atatggtatc acttagtaag 31500
aaacactttc taaaaaacaa tttatattag ccataattaa gaaaaaaagg gatattgaat 31560
aagtcaaaga gtggtttcca gggaagtctt tctttgtctg gaaagatacc ataggatttt 31620

ctgcagacag cttactcatt tttttcttga ttgaaatctg gaaaggaaaa cttgcaagaa 31680
aacattccat tctggactcg gcagcaggtc aagccaaagt ggcaacattt gcagcctgga 31740
gatcacacag tctgggagct caaacattta ggcaataaaa gctgatggaa gccaaaaagc 31800
cacgccactg gcatctggtg tcagggtagc tgctggggga gatctggcca tggtggtggg 31860
gcccagccat ataaacaagt tcagaggtag aactggagct gtgtactggg ttgaagcatg 31920
tctctcctaa attcatgttt tctctagaac cttagactat gaccttattt ggaaataggg 31980
tctttgcgat gtcatgcatt gcttaacatt gtggttacat tctgagtaat gtgttgttag 32040
gtgatttcat cattgtccaa acatcataga gtgtactcac acaaacctag acggtacagt 32100
ctcctacaca cctagaccat atactatatc ctattgttcc taggctgcaa acctctacag 32160
cctgttactg tactgactac tgtaggcaat tggggtacaa taatctaatg agactataat 32220
catatattta gtgtgccatt gaccgaaatg tcattatgat gcatgactgt agttaagatg 32280
aggtcatact ggattaggta ggttctaaat ccaatgtgac tagtgtcctc ataagaggag 32340
agaaacagac acaaacacag ggaaacaccg ggacgatggc catctgaaga cagaggcaaa 32400
cattggagtg atgcaatgac aagccaagga atgccaagga ctgcaaacca ttgccagaag 32460
ctaggaacac tcaagtaagg actcctccct agagccttta gaggaagcat ggctctgcca 32520
acccccttgat ctcatacttc cagccttcag aactgtgaga caatacattt ctattgtttt 32580
aagctatcca gtctgcggca atttgttatg gcagcctagg aaattaacac caggcatact 32640
tcagagcagg acaggtcaag ggataaccaa ataggtctcc tgttactaga attatttaca 32700
atgtcagagt agttcttgat gtttacttgg ccctctcttg gcaaaggctc tttgtatttt 32760
cctacactaa aggtctggcc aagtaggggt tcagattctc ttcaagtata gaaactcccc 32820
ccgatttta tgtttgctgg ccttccaagt aagatttcca ttgaagaaaa tgctccatgg 32880
ctaaaaagct ttaaaatcca ttggtattat cggcagattt ggactctata gagcctagtt 32940
tctaaagtgc ttcatagtgc cgatctgaaa gtgagatagc actagtccta tcagaggatt 33000
gttcaacctg agactctgca tcagaaggtc aggcagcact gacctgtgtc aggcctggag 33060
caggctctag gaggctgctt tcgtgatgag ttccttttg ttcaggagaa tataaggaag 33120
ctggtcctat tttagaagca ataacagcct ttgagtttgc tctagggcaa ttgcaaaatc 33180
aagagccccc agggtgctgt actccagatt tctaggtcac agatatccag accagagttg 33240
accagaaatt ggccagaatg ggttctgggg atgtggatga atttccattt ctcatccatt 33300
cctactccat ctccatttta tcattctcca ttcctactcc ctcaatacca aaattaaaac 33360
aaattgttga ttactaggta gccttcacat tgagttttc ctatggtata acccttgaaa 33420
aaaattgatc aaccagacca ttacaagaaa aaaaattatg gttttactga gttaagcctt 33480
ttactaggtt ttgcggtcca atttctctgt gtagacatag acttggaaaa gccaaaacat 33540

ctaagcaatg caaatttaaa caaattagtt aaatctgcca ctgggagtca ttatgtcatt 33600

ggcttttaac ctggctgcac attaaaatca tctgggggaa cccttaaaat gacttctgct 33660

caaagtcatg tgcccaaggt tgtgattaat ttgtcttcag ggtgattcct ccccttttaat 33720

atttctaaag ccactcaggt gacttgcttg tgcaaccagg ggtgtaatcc tctgatgtgg 33780

acatgtgact gcaatagagg aaaatgctag agagcagata ctctggaatc agtgccacct 33840

ggacttgaat cccaactctg atatctcata attatgtgac cttgggctaa cttagtctca 33900

ttgtgcctca gtttccttct ctgtagaatg ggaataataa tacctatctc ctagggttgt 33960

tataaagatt aaatgagtta atatgggcaa agtacttaga acattgcctg gaacatagta 34020

cgcaatatat aaatattagt tgtctgtcgt cctttgctga catttccctt actggatgtc 34080

tgaactgaaa ttgatctcaa tagtgtaata ttactccaac aagttatatt aacttcctgt 34140

gactgctgta ataaattacc acaaagtggc ttaaaacaaa ataaatctta ctcttactat 34200

tctgaaggcc agaagtctga aatcaaggtg tcagcagggc cacacttctt ctggaagctc 34260

tgaaggaaaa cctgctcctt tcctctttca gcttctggtg gctattggca ttccttggct 34320

tgcggtcaca tctctctttg cttcatcttc atattacttc ctcccctgtg tgtctttctt 34380

ctcctggtat ttcttgtata agaatccatg tgtttgcatc tagggcccac gtggattata 34440

caggatgagc tgcttttcta aggattctta atgtagtcac atcttttgcc atagaagata 34500

atattcactt ttttttgcta tcataaggta ctattcataa gttcctggaa ttaggacata 34560

gagatatctt tttggggtct accattcaac ccactataca agatggcata ataaaaagta 34620

agcttggatg ggaggcatca ctgactcatt ctgtgtttag tggacttcac atttggcctg 34680

cacatcccat tctctaatat gtctaaaacc attatttaca caacaggtac catccaaata 34740

tacaaacaag tgactattta ttgtcaatgt ttgtagttac ttctcggcaa ggacccacag 34800

aagtggagca agtgctcaga ggactggttg gcccaatggc ctttggcata tagagagctc 34860

caacaaggaa aggcttcctg gtggttttgc tccaaagaga acaatttttt gagaaactct 34920

attttgtgct aaaatgtgta cccaaaatct caccaatgat ggctgttttt tattttgttt 34980

tcattttaga gatatgatct cactatattg cccaggctgg ccttgaactc ctgggctcaa 35040

gagatcttcc tactttaccc tcccgagtag ctaggactac aggctgcatg actacgcctg 35100

gctaattttg ggtttacatt tggaaaagtc tgatgcttat tttaaaagag aacagggtga 35160

tgctacatta tcaggacatg ttttctgtcc caagtgatag aaaaatcaat ctgaataggc 35220

ttaagtgaaa ccctaattta ttaactctca taactggaaa attccagctt caggtccaga 35280

tcaatgcagt ggttccaaag atactatcag gacctggttt ctttctccag ctcttggctc 35340

tacttttgct ggctgtagtt tcagaaaggc cgtccttagg tactggcaag acaactgtac 35400

taagacctac attctctcag gttcaaggca catgaaaata aacagtccta gaaaaaaatg 35460

taagcaaaac cttaccgaga tttgttgggt tgaatactca tgcctgagac aaccaatgtg 35520

atagcacccc ttcctgttct gtttggccga ggaccttgga aaggatgacc cctcttaata 35580

catgggctaa gactgtggaa agaggtaggt ctgttctgaa gaaccagtgt aggtaccatc 35640

agaagggaga atgaatattg ggtggcaaat acaacagatg accactgtag atgcaattag 35700

gtccttggac taaaatgtct gaaatccaaa cctgggtttt cttgagcgac atgtgggatt 35760

ttttttttt tctagttgtg tgtgttggtc acaatttccc tttccacttg gaaataagtg 35820

agttattttg aagcagaaga cccacattta aattccatct ctgctgcctc tttgtagctg 35880

tgtggccttg ggcacattac cttatgtctg taagctttaa attcttcact ggcctggcgg 35940

taacacacac acacacatac acacacacac acacacacac acacacacac acacacacac 36000

acgatcagga tagaggccat cttaccagga ctattcatca ccagggcaca taaacagaat 36060

aagcctacat gaacacagtc tgattgatac cgaagaacca tctgtcccta catatttttc 36120

atggtcctga aacatgttgg aaatttctac catttgagta atggaaggaa tgtttaaagc 36180

aacatgtttc cagagagcca ggtgaaaaat gcaaattgat gccagggaaa agcaaaatga 36240

aatcctgcat cactgactac tccttatccg ccaccttaga agggatgagc caaagtcacc 36300

ttgtgtgatc attctcaaca tgcaaggcaa ccatcaagag acttcaggca aaatgatctt 36360

tctgtttttc cacatttgtt ttaggattct tctctaactg cttctcctga ggcagtgttc 36420

cctggggata tccaatacca cagggaatgt ccatattgaa aaactatacc tagagctctt 36480

ctttctccaa gttgtctcca gttgcaaaaa tgacctcttc atctccgtaa tcacagtgct 36540

cattttcaca gtggagttgc tattaggtag ggcaagtacc atctgattat gaattgatta 36600

aagcattcat attaagcatg tgtgagtgac aggctcaact tttttttcag ggagttagtg 36660

tttatcttca atcttctaga ttgaggtaag acatttttg agaaagatac ccgggtcttt 36720

ttccctttct cctagatcgg ttgcaagtgt actcacaaca gatgttatgt ggtattctac 36780

ttctaaaaga ctgttggccg taggttttag ctatcacttg gaagataaca agtagtagaa 36840

ttatccttcc tgttatgggt aggaaggaat tcctacggat aggaattatc tcaagatccc 36900

tcacagatgt gcactatcat gctccaaaag gtttattttt cctagaaatt gactagcctt 36960

caagtctttt cagttctctt atcaaaactt actactcctt tgtccaaacc ctttactatt 37020

cctttgtcca aacctccgta acccctgtta cagcagccac agggagctaa tataccttgt 37080

tggagttata ttagaccatt gaaatcaatt ttagttcaga catccagtaa gggaaatctc 37140

agcaaaggac cacagacagc taatatttat atattgctta ctatgcttac tattcctttg 37200

tccaaactcc tcaaatatcc ttcctttaga ttgcagagta gtattctgtg gtgtggacct 37260

acctcagttg aattggcagt tttatttttc ttcagctgtt tgaatgtgtc attccactgt 37320

cttctggtgt gtaaggcttc ttatgagaaa tctgatggta ttattgatgt gtccttgtat 37380

gtgacgtgtc acatttctct tgctgccttc gacaatttct ttgtctctgt attttggcaa 37440

tttgattgta atgtgtcttg gtctagattt ctttatattc atcctatttg tggtgctttc 37500

agcttcatga atctgagtgt tcatttccct tctggaattt gagaaatttt cagtgattgt 37560

ttctttaaat aagctttttt tcctattgtc tctctgcttt ccttctagaa tcaccataat 37620

gtatatattt gttgtcttga tgatgtctca tatgtccctt aggctttctt aactctttca 37680

ttctttttttc ttttgcactt ataactggat aatttcaaat aacttgtctt tgagttcact 37740

gattccttct taggtttgat caattctgtg tttgaagctt tctattgatt gtttttcttt 37800

cagcaattag attcctcaga tgcagaattt gtctggttct ttgtatagtt cctatctttt 37860

tactgagaat ctcatttttc aggtattact ttcctgattt cctttggttg ttcatatgtt 37920

tcctctcgta actcattaaa cttctttatg ataagtattt tgaattcttt gtcaggcatc 37980

taaaagatct ccacttctgt agggttggtt gctggagatt tgtttttttcc tttgattgtg 38040

tcatgtttcc cagatttttt atgtttcttg tagctttgcc ttggtgtctg cacatttgaa 38100

aaaacagcca tctctcccag tttttatgga gtggtgttga cagttaaaga ccttcatcaa 38160

ttagcccagc tagagatttg gagagcctct cacatagcaa gctgactgcc tcttttcctt 38220

tgttcttagc tgcccccatc aaactatact cattctgtca gtcctttggg ttgagtggaa 38280

cagggactgg cattcttctg gcaatgtagt gaaagaccaa gaggttggag gtatacacca 38340

ctcttctctc ttcttggtga gatgcctagg ttctgcaatt tctcccaatc tcacagagct 38400

ctgctatcct gtaacaatct gtttacgccc tttccattgt tgagttgacc gaggggtcca 38460

aactatggca gtactgtcaa tgttccatgt ggggcaagat agaaactgtc cccttggaca 38520

attcactgaa agactgggat gccggatggt cattccactt ctcttcccct cctaatgaga 38580

gaagtgtggg ttgaggcaat atcccttggc attgatctgt gctggctttg gggagaggct 38640

gacataggta aagtgtaatt gctcttctta tttgttttaa tgtggctgtt cttcattttg 38700

tgctcatcta ggatgcttgc aacttctcat aaaagtagtc tcacaaaggt attttggtgt 38760

gtatattatt gttagcttga tgtttctgtg gaataatgag gtgagggacc atttattcta 38820

ccatcttgct gatatcactc ccctgaagtg caaaagtttt aaattttgat gaagtccaat 38880

ttatgagttt tccttttatg gatggtgctt ttggtgtcaa gtctgagacc tctttgctta 38940

gtcctagatc ctgaggattg tctcctgact gaaaggctaa ttttcctcca ttgatttgct 39000

tctccacctt tataaaaaat catttgagcc tatttttatg gctctatttc tgggtcctat 39060

attctgtttt gtcaatctat gtgtctatcc caccaccaac agcacatagt cttgatcact 39120

ataactattt aataagtctt aaatctgata ggaactctga ctttttttttt ccaattattt 39180

tagttatcca agttcctttg actttctgta tacagatggt ccctgaaatt caacagttct 39240

acttaaaact ttttgactat atgaaggtat gaaagcaaaa tgcattcagt agaaaccata 39300

cgcagtgtcc acacactgtt ctgtttttca cttttagcac agtactatta aataaattgc 39360
atgacatatt caacacttta ttataaaata ggctttgtgc tagattattt tgctgaactg 39420
taggttaatg taagtgttct gagtaagttt aaggtaaagc aagctaagct gttatatttg 39480
gtgggttagt tgtattaaat gtattttcaa cttctgatat attgaaaaca atggttttat 39540
caggaagtaa tctcattgta agttgaggag catgtgtaca ttttagaatt atcttgtcta 39600
tatttttaa aaatttctgg gatgtaataa aaattgcatt gtcattttgg gggagaatta 39660
atatccttgc tatattgagt cttttaatcc atgaacatga tatgtcacca tttaaaaaag 39720
atctttaatt tattttatta attctttgga gttttcacta tagaaccctt gtacatgttt 39780
ggttagattt acaacaaaat atggtagttt tggggtcatc gtaaatttgg tgatattttt 39840
aaatttcagt gtcaacatat tcattagtag caaatagaaa tttaattgtg tattttgtat 39900
cctgcaaatt cactgaaata atctattaga agtgaggggt ttttttctgt atatttttgg 39960
ggatttccca catagataat catgtgattt gcaaatgact tttatttctc cttttctaat 40020
ctataaattt ttttcttacc ttattacact gactagaatt tctagcatgt tgttgaataa 40080
aagtagtaag aatgcacatc tttgtcttgt tcacgatctt aaggaaaaaa cattcagtta 40140
ctgactgttc gatataatgt tagctgtaga tgttccttat caagttcagg aagttttcct 40200
ctactcttat tttctatttc ttataatttt atcattaata gaaattgaat tttataaaat 40260
ttttaaatga ttgatataat caggttattt ctctttttt attctgttaa taaggtgggt 40320
tacatcaatt gatttttaag tataccagcc ttgcatctct gaactatatc tccagttggt 40380
catgctatat aattcttcat atagaattac tgaattctgt ttgttaaatg tttttgcatc 40440
aatttttatg gggactagta gcctgtaatt tttttcttgt tcttctttgc actgtcttta 40500
tctggtttat ctttaccttt ttttttttg gattagggta atacaagctt tataaaatga 40560
attgagaagc tcttctattt tttggaagaa atcacataga attggtatta attacttaaa 40620
tgtttggtag aattctgcag taaagccatc tggacaagga tatctctatt ttggggatat 40680
tgaaaattaa gaaataaatt acctagttta ttttttaaag tggttacaaa aaacaaagat 40740
gaatgtagtt tttaatttac cttgagactt ggtctttgat ccatgaatta tttaaaagta 40800
tgctgtttag tttctaagtt ttggagaatt tcttgttatt attatgtctg atctctgttt 40860
tgtttctatt atggccaggt gacatattct gtataatttt acttttaaa aatttgtcta 40920
ggattgcctt atgatataag atgtggtcta ctgtggtata tatcccatgg ccacttgaaa 40980
agaatgtgca ttctgctgtt gtttgatgct gtgtaataga aatgttgatt atatcttgtt 41040
ggttgatagt gttgttgagt tcttttatat ctttgctgat tttctagttt tcctagtttt 41100
ctggttttcc tatctatggt ttagaaatgg gtgttgaagc cttcagcttt aatagtagat 41160
ctatttattt ttccttctgg ttttgcttca tataatttgc cagtttgttg cttgatgcac 41220

acacatttaa gacttctata tcttcatggt taacttacca ttttatcatt atataatgtc 41280

cctctctaat tctggtaatt ttgtttgctc agagtctact ttatctgaaa ttagtatagt 41340

aactctactt cattttact tttaacattt attatttttt attgtggcaa aatacacata 41400

atagaactta acatttgaac cattttgagt gacattaaat acattcttaa tgttgtgcaa 41460

ccatcacttc tatttagctc atgactcttt atcttataaa actgaaactc tgtacctagt 41520

aagaaaataa ttcacgcctg taatcccagc actttggaag gccgaggcgg gtggaccatg 41580

aggtcaggag attgagacca acctggctaa tatggtgaaa ccccctctct actaaaaata 41640

caaaaaatta gactggtgtg gtggtgggca cctatagtcc cagctacttg ggaggctgag 41700

gcagcagaat cgcttggacc tgggaggcgg cggttgcagt gagccgagat tgtgccactg 41760

caccccagcc tgggtgacag agtgagactc catcttaaat aataataata ataataataa 41820

taataataat aataataata ataattccct ctacttccag cccctggaag ccaccattct 41880

actttctgtt tctatgcttt tgactacttt taactacctc atataagtga atcatatgga 41940

atttgtcttc tcgtgactgg cttatttcac ttagcacatt gctctcaggg ttcatccatg 42000

ttatagtacg tgttagaatt ttcttccttt ataaagccat tgtaagtata taccacattt 42060

tgcttatcca tttattcatc tgtcaataga cacttgattg cttccacatt ttagctattg 42120

tgaataatgc ttctatcaat gtgtgcacaa atattgcttc aagaccctgt tttcagttct 42180

tttagatgca tattcagaag tggatttgct atgtcatgta gtaattctat ttttaatttt 42240

tgagtaacca ccatattgtt ttcctcagtg gctgcaccat tttacatttc tactatcagg 42300

gcacaagtgt tccagtttct ccacatcttt gccaagactt gttatttttt gttttcttaa 42360

tagtagccat cttaattggt ttggttggag atggtatctc attgtagttt tgattttaat 42420

ttccctaaag attagtgatg ttgagcatct tttcaggttc ttatgggcca tttgcatagc 42480

ttctttggag agacatttat tcgagtccat tgcccaattt tttgttgttg ttgttgagtt 42540

ttaggagtgc tttatatatt ctggatgtca atctcttgtc agatatatgc tttgcaaata 42600

ctttctccca ttctgtgggt tgccctttc ctctattaat agtgtctttg atgtacaatt 42660

ttaaagattc tccatgaagt tcagtttttc tgttttttct tttgttggct gcacctttgg 42720

tagcatatcc aagaaatcac tgccagatac agtatcatga tgcttttgtc ctacgttttc 42780

ttttaagaat tttatagttt ttttcttata tttaggtctt tgatcaattt tgagttaatt 42840

tttctatata gtattaggta agggtctaat ttatttattt tgcatatgga tatccagttt 42900

tcccagcatg atttgctgaa aagactgttc tttctccact gaatggtctt gacatctgtt 42960

ttaatcaggg ttcttcagag agacagaatt aataggagat atatatctat atctatatct 43020

gtatctatct aactatatct atatctatct atctatctat ctatgtagag agaggcgggg 43080

gagatataag aaaggattta ttaggggaat tgactcactt gattatgtag gctgagaagt 43140

ttcataacag atcatctgta agctggagtg ccagggaagc tggtagcatg gctcattcca 43200
agtctgatgg ccttagaacc atggaagcca atgttgcaat tctcagtcca ggactgaaag 43260
cccgagagcc tggagaattg ctggtgcaag tcctaaagtc caaagaccag agaatctgaa 43320
cttgtctcat gatacaaata taatctacca tggtatatag cccatgtaca cttgaaaagg 43380
gtagaagaaa tgaattctgg ctccagaaga cagatcaaga atttgtcctt cctttacatt 43440
tttattccat cacccacatt gagggcagat cttctccacc cagtccacca actcaaatgc 43500
caatctcttc cagaaacacc ctcacagatg cacctggggt agcccaatca ttagaatcaa 43560
atgctaaatc acttgggttt ccctttttaca gaagggagac atgatcagtt tctactgaag 43620
cattgagaat aatttgtact ttatcagctg ctgggtatcc cttaatccag tcaaggtcac 43680
atccaaaatc aaccatcata gcacccttgt caaaaatcat ttaaccatat atattagggt 43740
ttatttctgg actctgtatt gtatttcaca ggtctatgtg ccttttagac ttttatttt 43800
atttttattt tattttattt tatttttga gatggagttt cactcttgtt gcccaggctg 43860
gagtgcaatg gcgccatctc ggctcaccac aacctctgcc tcccaggttc aagtgattct 43920
cctgcttcac cctgcctagt aactgggatt acaggcatgt gccaccacgc ctggctactt 43980
ttttgtattt ttagtagaga cagggtttct ccatgttggt caggctggtc ttgaactcct 44040
gacctcaggt gatccgccct ccttggcctc ccaaagtgct gggattacag gtgtgagcca 44100
ctgtgcccag cctattttta ttttttttaa ctttaaaata aagttgaggg ggcacatgta 44160
caggtttatt acatgggtaa gttgcacgtt gctgaggtgt ggtgtacaaa cgatcccatc 44220
acccagttag tgagcattgt agccaactgg tagtttttca gcccttagcc ccctctcacc 44280
cttcccactt tattagtccc cagtgtctgt tctttttgtc tttatgttca agtgtactca 44340
acgtttagct cctacttata agtgagaatg tgcagtattt gttttctgtt cctgtattaa 44400
tttggctttg aataaaggcc tctagctgca tccatgttgc tgcaaaggac ataatttaat 44460
tttttatggc tgcatagtat tccaagatgt atatgtaaca tattttcttt atccagtcct 44520
tcattaatgg gcatctaggt agattgcatg tctttgtctt tataggcttt tattgtctat 44580
atgccagtac tatattgctt tgattactat agtttttagt aagatttgaa atcaggaaat 44640
gagagtcctc aatatttttt ctccttttttc aaaattgttt tggctttttg atgtctcttg 44700
agattccatt tgaattttat agtggactgt tttatttctg aaaaaaaaaa gtcattggaa 44760
ttttgatagg gattgtattg agtcaataga ttgtgttggt agtatggaca tttgaaaaat 44820
attgtcttcc agtccatgaa catggaatgt tttccatttt tatattcttc tttaacttct 44880
ttcagcaata ttttataatt ttttactgta caagtctttc acgtctttag ttaattccta 44940
agtattttat ttgttttgat gctatcgtaa atgagacttt cttaatatcc ttttcatatt 45000
gtttattgta agtgtataga aatgcaactg atttttgtgt gtcaactctc tatcctgcta 45060

ctttgcttaa ttcgtctatt aacagttttt taaaaatgta tgtggaatcg ttagagtgtt 45120

ctagacacat gatcatatca tctgtaagca gagataattt tagttccttc tttctgattt 45180

gtatctcttt gatttctttt ccttgtctaa ttgctctggc taaaacttct agcactatgt 45240

tgaatagaaa tggcaaaagc agcacccttg ccttgttcct gattttaaaa gaagagcttt 45300

catctttgag tacgtttgct ttgggttttt aatatacaga ttttattatg ttgaggaagt 45360

tgccttccat tctcagtttg gttggtgctt ttatcatgaa agagtgaatt tttcaaatgc 45420

tttttctgca tcaattaatt gaccacgtgt tttaccctct gtaagcctga caacgctatg 45480

gattacactg attgattttt gtattttgag ttatccttgc attctagaat taagtcttac 45540

ttgatcatgg tctataattc tgtttatatg ctgctcaatt tggtttgcta gtattttgtt 45600

taaaaaattg ctttgatgtt cataaaaaat actgctctat aattttcttt tctgatagtg 45660

tctgtgtcta aatttggtgt cagaataatg ctgacctcat agaataagtc aggaagtgtt 45720

ctctctcctc ttcatttttt ttttggaaaa gtttgagaac aattggggtt agttctttaa 45780

atggtagaag tatttctact attggtagaa ttcaccagtg aaactgttag atcaagggct 45840

tttttttca ttatgagatt ttgatttttg attacttatg taatctcctt actagttata 45900

agtcttttca aattttctat ttctttatga tttagtcttg gtaggtttag tatttctagg 45960

aatctgaact ttttcatgta ggttatccaa ttttgggggg tacaattgtt catagtgctg 46020

tcttagaatt ctttttattc ccatagaata agtagtaatg tcccactttt atttatgatt 46080

ttagtaatat gagtcttgtc tctatttttc ttagtcaatc taagtgtaga attgtcattt 46140

ttaaaaaaaa tttttaaaga aggagcattt ggttttattg gttttaccct tgtttttcta 46200

ttcttgattt ctttgatctt tgttctaatc ttaattattc cttctttctg gtagctttgg 46260

gtttagctta ttcttttcta gctccttaag ttgtaaagtt agttggctga tataggatct 46320

tccttgtttt taatataatc atttgtagtt tcaaatttca tgcttaacac tacttttgct 46380

gcatcctata agttttagta tgttatgttg tcattttcat tcatatctaa gtattttcta 46440

atttcccttt gctttctctt ttgatccatt aatttttta aagaatgtgt tttaaaattt 46500

tcacatattt atagattttt cagttttact tttgttattg atttctaact ttatcctgtt 46560

gtggtcagag ttgttttgta tatttctgtt agatctagtt ggtttattgt gttaagttct 46620

ctatgtcatt acttatattc tgtctagtta ttctattcat ttttgacagt gtggtattga 46680

attctttaac tattattgca gaaatgtctc tttttacttc aattctgaag ttttcactgt 46740

ctttattttg atggtctgtc attaggtgca taaatgctca taagtcttct atcttcttgc 46800

tatactgaac cttttaagat taagtacttt ttttgtttct tgtaaccatt tttaaaaaaa 46860

tttaaagtcc attttgcctg ttagtacagc cacatctgct ctttttttcat ttccatttgc 46920

atgaaatgtc atcttccatt tttccacttt caatttattt gtgtctttgg agctaaagtg 46980

agtctcttgt aaacagcata tatttggatc atttaaaaaa tccattctgc tcatctatat 47040
tggttgaaga gtttaataca ttttcatgta tgctattact gaaaaggagg aacttacttc 47100
tataattttt atatttgttt tctctacacc gtataactcc ccatcccttg ttccctttg 47160
tatatattct atagctattt tctttgcagt taccattgga attacattta acatcctaaa 47220
tttataacat tctaacttat aaaccagctt aatttcaata acataaaact ctgctacttt 47280
aacagctcct tcccatctct ctttgattgt taatgtcaca aaattgcaac tttatatatc 47340
atgtgtcaca aaacataaat aattccttga aatgcattaa actcttctat ggaaaaaata 47400
atgagttaga aaccatagtt tcagtgatat taacttttag actaataatt gttttttaa 47460
aaagtattag tttcttaaat catgtacaga acacaaagtc aagaaacatt gttataataa 47520
taccaccttt tacaatgtcc ctatgtttac cttcattgat atttttattt ctttatatag 47580
attctagtta ctgtatagta tgctttcatt ttaacctgca ggactccctt taacagtttt 47640
ggcatggcag atgtagggca gcaagctatc tcagcttttg tttagctggg aatgtcttaa 47700
gtttctcctc actttcaagt tttgccagat atggtgttct tgcttgacag tttctttttt 47760
atattagcac tttgaaaata tcagcccact gccttcttat ctctaaaatt tctgatgaga 47820
aatttgtaga taatcttatt gcagatgctt ggtatgtgac aagtcatttc tatctcttgc 47880
tgctttcaag attttctctt tgcctttgta tttggaaagt ttgattataa tgtatatcca 47940
tgtgggtatc tatgaattca tcttacttgg agttaattga gcttcttgga ggtttatgtt 48000
catgtctttt ttcaaattcg aagaattttt caccattatt tcttcctata ttctctctac 48060
tcctttcttt ctctctgcgt tgtctgggac tctcatggtg tgtatgttga gcccccttgat 48120
gatgtctcac aggtctcttg ggctctgctc acttttcttc aattttgttt tctttttgtt 48180
cctcagactt gatgatttcc attgccttat ctttgagttc tctgattctt tcttttgcct 48240
actcatatct tccctcaaag ccctctagta aatttttcat ttctgttatt ttaattttta 48300
gctccagatg ttctttttag gttttcaaaa tctttatttg tattgtcatt ttgttttata 48360
cattgttttc ttgacttcat ccacatgtac ttttagttta tttatttatt tatttattga 48420
gacaggttct tgctctgtca tccaggctgt agtacatggt tcagttagct cactgcagcc 48480
tcaacctcct tggctcaggt gatccttctg ccttagcctc ttgagtagct aggactacag 48540
gtgtgtgcca tccatgcctg gataaataaa taaataaatt taatagagat gaggtctcac 48600
tatgttgcct aggcttttaa attttatttt ttgggtatgt agtaggtgta tatattcatg 48660
aggtacatga agtattttga tacaggcatg cagtgcataa taatcacttc taagatacaa 48720
aataaagccc tctttactct ttgctttcct ttccttaagc agatggtggg agtaaatttt 48780
gttgtgagtt gtgttgcctg gtgttgcagg aggaatggca caagcacttc cttagccacc 48840
ctggctggtg tccaatgttc actgattcta agcccagcac agcactagga cttgcccagg 48900

aattgcagtc cttgtggcct agactgcctc tcaagtttgt ttaggatccc agagcactta 48960

agcccatggt ggtaagtctt gtgaaaattc aagttccagc tgctgggatg ggtgattccc 49020

ctctggctag ggctgatcta tatgctccct gtgtgtgttg gcattggctg agtttagccc 49080

agctttactt tccattgtga cagggcagca ttgagttcaa tgcagagccc cacaatcact 49140

gtactgtcca tttcccaggt ttacagattg tctctctgtg ctatgtggct gctgccagag 49200

ggatagggga ggggcatcat tggcaattca agactatgtt tcttaccttc ttcagtgcct 49260

ctttcagcaa tatgaagtta aaccaagtac tgtgattgct tatctgattt cctgttttta 49320

cgaaggtgct ttttgtgtgt gtagatagtt tgttaaatag gtcttctgca gtggggatca 49380

ttgttgcaag gttcagtttg gccatcttgc tccaccctcc ctcttttcca gttcttaaag 49440

tatcttcaag acagttattt taaagtcttt tttgagtaga tctgctgtta ggtctttttc 49500

aggggcagtt tctgttgact attttttcct ttgaatgggc tatattttcc tctttttttt 49560

ttgaatgcct tgtgtttttt tttgttgaaa gttgggtatt tcaatttaat gatgtggtaa 49620

ctctgggatg cagactcttc tttttcctca aggttgtttg ctttttgtta ttgttttgtt 49680

tgtttataaa aattgcttta gtctgtctct gtgccaagga tcagcctgag gtgtaaacat 49740

aaggtcttta ctggtattct ctgagcttgc atctttctgt ggtcatgtgt gttaactttc 49800

taattttccc catatattca gttgtttgtg aatgtcctta tctttaatat ctggctccca 49860

aaaggagaaa aagagaaaaa tgaaaaaggg agtggaaata gggtgccagc cctttaaatc 49920

tctggaagtc atttcagctg gatggggagg ggtttgcaac aatggaataa ggtgtaacag 49980

caaagaccca ccacctcttt gtctgtacct ctctgatcag aagcagcaat catcaatcta 50040

agcacatatg cctgatactt agaggacagg gtccattttg cttatcctgg ctccttcaag 50100

ctgtgtgcaa caagctgctg caggaataca tgcacagctg cctgccacag gggtggggat 50160

aggaaatggg tagctgttac tgtgctaaga gctaaaattg actgagctga aatcaaagtt 50220

aactgcaatg taccatccaa atgtttccct gaaagttgca agccttcaat agactccaga 50280

tttccaaaac agttatatca gacatactct gtcagtgcaa ttattgccta agcagggaga 50340

cagattcctc gtgtttctta ctcttgcagt tccccaggat gctctcccta ccttccttta 50400

tttaatgttt ttatgataca tcttttcccc tttttattac gtttaccctg actatattgt 50460

tatatttgag tgagtttctt gtcatcaacc tattgtttgg ttatgtttta gtcaactctt 50520

gtcttttaat tgtctttagc caactcttgt ctttacaatg atttgaatta tttacattta 50580

ttggatttat taatgtatta atgcttaagt ctgaaatttt atttttttgtt ttatatttgt 50640

tctctctgtt tttctatgtg ttttcttttt ttatgcttcc tggtgattat atgaatattt 50700

tttagaattt cattttgatt tatccttaga tttgatacaa gagaatctct ttcatatagt 50760

tttttagtga ttgctcttgg tgttaaatta tatatgcaca atttttcata gtttaaaagt 50820

gttgtcattt taccagtttg agtgtagaaa acatacttcc cgtaatgcca cattttttctt 50880
cctcatttat aatataattg tcttaaatat tccccccttcg tacatttaga attacataat 50940
acagtgtatt ggcatctatt gatttttaaa aattcagttt gagaccttct tggttcttgg 51000
tatgttaagt tattttccat tgaaacctgg acattttgaa acctgaacgt ggaggctcct 51060
tgttactttt gtgtggcggt ggggtttttg gctccctgtt agtcctccac tgatatctgt 51120
ttggctgaga gagttgggaa tgtttccttt cacctcccaa ctggtttcca ctgacaccat 51180
ggaatgcagt ggaggaggga aggtggcctt gttgtcactg ggaaacggtg aatattccaa 51240
ctctccacta gggcttctct gatactaccc aggccagcag gaggatgtgg agttaagaaa 51300
tcctggctcc ccatgttgtc tctactaaca ctgtggagaa gtgggatgag cttgttactt 51360
cccagtagga attcctgact ccctacccag ccttttctga cacagcctgg caaggggtta 51420
gagtgcctat aacagcttgg taaggggggaa gcacaggctt ctgcacttcc atcagacttt 51480
gctagtgggg tgagagtgag ccagtttttc tgtggtgttt gttataacaa agcaactata 51540
ttctaaaagt ttttgtcttt ctggtttttc ccttttttctc attccttggc tagagaaagt 51600
aagattttgt ttggcctttt tgatctgtga tggttccatt ttatggttgc caacttcaat 51660
ggctctaaat ctggaatata tgaggcaaaa tgaaaatcca ggaacacact gctttgtttt 51720
tcttcaaatc ctaaggtttc tagcccatat gccttgttct ctccaacttt tagaatcttc 51780
tcatgtttgc tttttaaata acgtccagag actcaattat atgtagcagg aggaatgtgg 51840
aaaagcatct ccacttcaca ccccccctgga agtaaaagtt atgatgcata tacagtgaga 51900
taaaatttga agctctgcat gcgtatgatg tgtgccactt atagcacatg atagactctc 51960
tttcattcaa aattcattcc aggcctgctg tgtcccaggc actgttcaag gcattgcaga 52020
tatagtgatg aacaaaatag ataacatttc tctctttatg gtgcatacat tcttgtggga 52080
agaggtggac aataaacaca gaaagtagaa tatgttagta aaaaatgcta ctggaaaaag 52140
taaagtagat ttatgaggct agtgagtgct ggaggcattg gaggttattt attttacata 52200
aggtggtcag ggaagctaac atttgagcag agtggctgca gtgagatgga caaagacaaa 52260
agtggtagaa gagagcagag atgtagttgg ggaatcagat tgtctagggt cttgaaggca 52320
gtcaagaatt tgggctttca tttagtcatg aaggaggttt tcagagagaa gtaatatgat 52380
ccagtttaca gctttattgg tctgctatat ggagaataga ttgcggtgga gtaaatgtgg 52440
tggtcaaatg aggaggcttt tacaaatacc cgggagaggt ttaatgagag attaaactca 52500
gatggaataa tggagttagt gagatgtggc cagattctga aaacattttg cagataaaga 52560
tgacagaaat tgctaacaga ttttatgtgg ggtgtgagag aatgagagag agagagagat 52620
caaagatggt ctaagatctt tggcttaagc aattggaaga ataaacttgg catttactga 52680
gatggggaag accgagggaa gtgcaagtct ggggaagaat ggggagtcag aggtttgggt 52740

ttgactgtgt taaaattgaa atatccatta aactaggggc atagtaggag gttgcccaca 52800
ggagtctgag tttaaggact gcagatatcc tgtctggaga tatcaatttg ggacttgctg 52860
tcctatagat aattgctttt gtctgttttg cgctgctata actgaatacc tgagactggg 52920
taatttacaa agagcagaaa tctatttcac acggttctag aggctgggat gtacaaggcc 52980
aaggtgccag catctgatgg actccttctt ggtgtattct cacgtggagg aaggcagaag 53040
gtgaaagggc aagaatgaac aaatccactc cctcaagtcc tatttatagc agcattaatc 53100
cattcatgtt ggcagagccc tcatgaccta aacacctcct aaaaggcccc acctttcagc 53160
accgttgcat tggggattaa atttccagca cacaaatttt ggggaacaca ttcagattat 53220
atgaatgata tttaatgata tgtctagatg tgatcacata gacagagact gtaaataaag 53280
aagaaaaaga gtcctgagtt ctgggggcac tctcatattt agaggtcagg aggatgagga 53340
gaaaccagca aaggaaaatg agaacagatc agtgaagcag aagaaccaag agagtgtggt 53400
gtgctggaag ttgagtaaag aaagtgtttc cagaaagagg gagtgattaa tttgtcaaat 53460
aagaagagag ttgtaaattg attcttgggt ttgggaatgt gatggtctct ggtggcccca 53520
ccaagatttg tttccatggg aggaggggga aggaggaaag aagtggagga gaagacagag 53580
atggtgagca taagcaactc tctggagttg ctataaagga aagcaggaaa atggagtagt 53640
agatgaacaa ggttacaggg tcaagaaagg tgtaattact atacagaaca gttaaatata 53700
tacatggaaa ctttgtattt atctatagag tttgaattta ttttgattga caatgagtct 53760
aaaatttcat atagtgaaaa gtcttcaatt ggcttgataa tcttagcaat agcatttata 53820
tttgaagaag acttagttaa atatgagttg gtctatgcaa gatgtgtaat tttaaagctt 53880
cttttctttg gtttaatttg gatttgcaat ttcagttaac cctttccaat gaatcccccc 53940
aaatgaatat ttacttagca atgataaaaa aactttatat ttacagagta cttatcagtc 54000
tctctataag aacaaacata aaagaatgaa aatttacatt agaggtgtag gaggtaatta 54060
aagtgatgtg gtcccaaacc agggaaactg agtctcagac cataggtgga gcatgggatc 54120
tgaaggggaa actcacctac aactctacag caccaattgc cagcctcttg ggctaataga 54180
ctctctcccg cttctgtcat tgtctttgtc tttttctaca gtgaaacaag ctttgaacta 54240
tttccagctt tccaatagca aagttattca gattagatga actttatttg ttctccggga 54300
catctagttc tccaaagtct tctgtctgta ccatgtgttc accaaacctc cttctttttc 54360
ctgctgggaa acccaatcag ctgcatttcc cagcctccct tgcagttggg tggggccaaa 54420
agaatgaggg tggaatttat gccacttcca gcctgaagca tggtcattaa gaaaatcttc 54480
tacacaatcc tccttgtcct ctctcttcct ttgcctgctg gatagatgca gaagattcct 54540
tggaagggcc tgggtcctga atggctgtgg agcagaagct tgaatagcat cttactgtgg 54600
catgagcaag aaatgagctt ttattatgtt gatcttttga tactttgtag ttgtttgtta 54660

cagtagtgag cctgccctga ttaatacata cttctactgc aagtattaca aaaatacaac 54720
tttttaaaaa ataccttttct gtagcctttc aggatccttt ccttctaaga agtcaccttc 54780
aggctcccaa agctttcctg gagtgtgaat gcaaggagaa acaaatagca acaatcctgt 54840
atcagttact ttttcctgca tcatcttatt taatttctgt aggaatccaa tgattctcat 54900
aaaacagtag tccaatgagt ccagcctcat aatccaataa ggttaataat taacctcagt 54960
ttacagatga aggagtttgt ccaagatcac agagttatga aatagtgaaa tccttcgagc 55020
ctgacctttt taaccacgga gcccttgctc tcccactaca tcttcactct gttcttttc 55080
cctctgggga aggaagtaaa actcatgaat ctaattcact tatgcacact ctggtattag 55140
agactcaatt tcctttctct tgttgtgtgt atttgtgttt tgaaggaggt gagaaacaga 55200
gaaggtaatt atttactgac atgaattgta ggcactgttg tgattgggtg gggtgggagg 55260
cattctgcag acgacatagt agacctgagt ccaggtgtga aggggagagg gagacagcag 55320
acagcattta gtttctaggg agacagcaca ggaaactaac ctttctttcc ccttcagctt 55380
tttaatacaa ataattaaag atcctcatag tccattaact ggccaggaga gcagatggta 55440
gaggtgagaa gtttcagcat cctgagaaca cttgagcagc ctccctgttc caacagaatt 55500
gtccatattc aagccaagag aggaaagatg tggaactgct gttgccaagg gggaaagtgc 55560
aggtcttcaa taccaccttg atgttttatg tttataaaat ttggctcagc tgggcgcggt 55620
ggctcatgcc tgtaatccca gcactttggg aggctgaagc aggtggatca cgaggtcaag 55680
agttccagac cagcctggcc aatatggtga aactctgtct ctactaaaaa tacaaaaatt 55740
agctgggcat ggtggcaggt gcctgtagtc ccagctgctt gggaggctga ggcaggagaa 55800
ttgcttgaac cctggaggtg gaggttgcag tgagccgaga tcgtgccact gcactccagc 55860
ctgggcaaca gaatgagact ctatctcaaa aaaaaaaaaa aaattgactc acacataatg 55920
caacacctgt ctgcatactt ttgccagtca ctccataatt taaaatgtgc ttcttcatag 55980
gaagcatcaa attagataat ttcatcctca cagcaatttt aggaggcaac actcacatat 56040
gatccaggta aaaaaaatgg tgactcacat ccctgacatg aagcccaggg catttcttag 56100
acttcctgtt tttgagaagg aaatctaaga caaacctccc agactttgaa ggatgggtgt 56160
tcctatccaa aatgcaactg tgattatctg tgaaatctgc agatcttgtc tgctctttct 56220
tgtctgcaaa agatcagatg aatgctctgg agatgtgtgt ggttgtctag catgagcatg 56280
tgcgtgtgca tttgtacatg tgtgtgtgca tgcatatgtg tgtgtgtttt tgtgtaagag 56340
acaaagaaag aaaaatgaat ataaaattta cagaatcaaa tatcagtttt caaagcttca 56400
agatccaatt gtgtgtatag gattatctgc cctgtttagg aaagtgtttt ctggagtgga 56460
gctccaagtc tgtgatgaat gtgccaaact aggggttcct tctcggagag tcatcatatc 56520
cttagtatgc catggcttga agaaacccca caatgagtaa atattaggtc ttgtctgatg 56580

ttatagatcc caagcttact taactatgga ttctcttttt tgagtctatc actcattcac 56640
atacagtgac agtacatctt tttgaaaatg ccaattcaag agtaattaga aaggtttaat 56700
gtagaaaact aggattatca gaagacctag attttgctct tactctatca ctaataggct 56760
ttataatttt tgataaatta tttttattta gttctttttc aagtattttt ttctgccttg 56820
aaggaaacat ttctttaagg atatttattg tacttattta aaattgttgt tctgtcatga 56880
taattccact ttgcatggta catgttattc attatttatt acataaatta tttatatatt 56940
acatgttgtt gattatttct tagtggttgt acttttcagg tatgtaatta ttttggcctg 57000
tgatatacat cctcctggag aagataattt gtattgggtt aaggcgaaat ggcagagcct 57060
ggtttttgta ccttctggtg tgagcttaag aaagaggtgg ggatgagacc atgttctttt 57120
ttaacagtga atcctaacct ttcctccctg tgtgtcccag gacatttgtg tactcactgc 57180
tcaatcgagg gaggccttat ccagctatac tcattctcag aggcactgcc ttctgcactg 57240
gaaatggagt ccttcaaggc tactatctga tttactgtgc tgaataccct gatgggtggt 57300
acacagacat acggtttagc ttgggtaagt gaatctgccc acttctcacc tacttcccag 57360
ctaacaaccc ttcccacaat ctacatcgcc atggcctctc cctactgcaa tgacctcgta 57420
atgatcccat cttcccctcc ctcacctcta ccctgatctt ttctctatat ggtagccaga 57480
gagattgttt aaacacatat catgccattt cccatcgcaa aactctccag tagatttcct 57540
ttactctcaa aataaaatac aaattccttc ccactgcctt taaatcctaa atattcttgg 57600
tcttttcaat ttcccaacct cttttcctgg ctccctgcac ctccttttct gtgctccagt 57660
gccagtggcc ttcctgctgt gccacaagct gtcaagcttg tccagcccca gtgtttttgt 57720
ataggactgt tccctctgcc tagtacaggg gtgtccagtc ttttggcttc cctggaccac 57780
attggaaaaa gaagaattgc cttgggctac acatataatt cactaacacc aatgatagct 57840
gataagctga aagaaacatt gtttcttaaa acaatgtttt aagaaagtgt acgaatttgt 57900
gtcaggccac atccaaaact gtcctgggct gcatgtggcc cacaggctgt gggttggaca 57960
agcctggcct agaaggcttt gcccccatgt attcatgggg gttggttcct cactttattt 58020
agttccctac caatttgcac ctcctcaaag ggactttccc tgaccaccct atctaaaatg 58080
gttgaagaca ctgctgtgtg tgctgtcccc cttccctccc cgctccccta ccatcccctg 58140
ccccagatac cctttcttcc aggctaatga tcttttgact aggcaaggtg gaaaatcctt 58200
gttttatatc aaatcaaata aggtgagaat agacttgatt gtttcaacta aactgttctt 58260
gctttttgcc tattttgaaa agcaccaaag tgctttgctg acaggttggg ttgggcctct 58320
ttgtgggacg gtgagtgttt ctgggctgta ataatgcctt ttgggatgca ggatctagca 58380
tccctgatcc tggctgtcct cacctcagaa cagggccctt tctgtaccag tggatagtgc 58440
atgtggagac acctccagga tatgtggcta agtaagataa ataaaaatgt gaacagtgtg 58500

tgtagtatgc tacttttaat gtcagaatgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt 58560

gtgtgaactg gcagtgatgg aagtcagttt gttagtggcc acgcctccaa actagctcac 58620

gttatttcat gagagtgggt gtttcagtca ggaatgcgtt cagaaaacca tataatagtg 58680

acgggaataa ttcagaattc atagttctta cataacaagt gtcgaagtag gtggcttctg 58740

cattcctgtg gttgcttact gacaccatta ataactcagg cactttgtgt ctcccctatt 58800

cttagcatgt ttacctgtgg tcctcttatt catcacttca tggttgcaag atgttgactg 58860

tagctcaagg cattacatct ggcaatcaag acaggaagaa agacgaagta ggggcaccgg 58920

tcttgcctgc acctttttatc agaaaagcaa acgatttcca aggaagtccc ccaaccaaga 58980

cttcacttta catcttattg gtggaactag ctcatgtgac ccccttttctc agtgcaacct 59040

ctgtagtggg ggatggcaaa agaaaagggg ctggaatcag ctgttgagat atgaaacctc 59100

gatttgactg tttgtgaatg agctaaaggc ttactattat gatccatgca tttgtttgtt 59160

tatctattta aatactggac aatggtgcta cctcctgctc tcctctcttt tctaatctgt 59220

ctccatcagt ggtgccactg tgtactttca gcccaagtct aggaaacagc acacccagtg 59280

ctccccattc aggaccagga ctcattgccc tccccacttt ctgccacgtc ttaggaccat 59340

tcttagattt agaaattaaa tgcccctcct ttcattttag cttagtttgt gaaaaaagca 59400

ccacaatctg gacacattta aaaaaaattt ctcctttctc tcttctttgt caaggtgtct 59460

tcttatttat tttgggaatg ggaataaaca ttcatagtga ctatatattg cgccagctca 59520

ggaagcctgg agaaatcagc tacaggattc cacaaggtaa tgtctcccct gcccccagac 59580

tctcactctt ccctggagcc tgtcccaggg atgatgctat ggtagcagat ggagagggga 59640

cagtgagggc acgaatgata caatacctct cagcttgctc ttgacttccc ctgcaaaccc 59700

agtcccatca cagtacctct gcatttctaa tctgaaccca gaagctccag agagctacca 59760

gagccctcag gaaggtgcga gaccgcaata cccggaaggt gggagagagt gggagatttg 59820

agtagggttg gaatcggcta cctacaccct cattgcagta ggtaaggttg tcatgtacag 59880

agggctgatc ctttctaggt tgcaaatgat gctgaatgct tggccaataa atgtgtcccc 59940

tccaattgat ctagacttat cttgtgagca gttaaggcta gaacttgcgt atttcctgcc 60000

attcatatat acttttaaag gtgtagagaa ctatatttac ttaatcaaaa cttaggatgg 60060

gaggccttac aagcacaagt gcatttttgg agataaaggt gagcatgttt gtaatcctaa 60120

ctgctccaaa gaaaccaggg tatgagattg acaaatatac gcagatggga gcaaatcagt 60180

ccaagtcatc cttcagtagg tttagatggg tatttgtgta ggtccttggc ttccaccgtt 60240

tttgatgtaa atacaaccct ttatttacat caaaaaattt cctcaattat gacatgatgt 60300

tagtgcacat taatagtcat tgattaagaa attaatgaca aagttactat gaattcagta 60360

acagattcaa atgaatttga atgttgttaa tatcctaaca gtatctacat caaacaaaaa 60420

taatttagga ggttaagatg tgccgtttac tgtcttcata gaaaatttat aggccctttg 60480
ctttagatcc gtggttcctc ccagggcgta gggaatcaca ggttgggaac cactgacgca 60540
gtctcatctt caagaaagat tcaactctaa ggggctttga ttttaaaaac attcactcca 60600
taactagata aataaagaag agcagagaaa gcacttgaaa accagttgcc aagattagtt 60660
tccaactttt gaattataat agagaatgat ttaaaacaaa gtatttttat gtaactgtag 60720
aaagaacaaa attgtttcgg ttgaaacatc cccagtttaa tgtgggtaat aaaatttagt 60780
gtggatatat ttaatatcat tagaaatatg ctgatttcta gatacagtcc tgagagaaga 60840
aatacctggt tggatagaaa atgaaacatt taaaatctag aagccgactt caccagccta 60900
cagcaggaca aatacctgca gctcctactc tctgctttaa acatgaacag aggagagtgc 60960
tttgcagaag ggtggggagg ggcaaatccc ataagagaat ctaaattcct tctcccgtga 61020
gttcagattt ttattatttt aatgtagtgt gcagtttcac attttgggac tgtgaatgtg 61080
aacgtgtgtg tgtccaggaa aggagcgggg aggtaagagg tggcccaaaa accttcctta 61140
acagaacaaa acaaaaacca gacctcctac acctctccct tatcctaccc aaagctagtg 61200
gtccagcagt tgttagagat ttggatagag cccgttaagc agttgaggcc actcttcgca 61260
actccagaat gttctccagg caacaggctg ttgttgcttt gtttcccctt ctccccaaga 61320
ggattccacc aaactcctat gactatggag ggagcctcca gccccacatt tgttcttgct 61380
gcctttgtgt attttggaac aacacagatg ggtttaatgt caaaatgatt cagttgcaat 61440
gattgacctt ccgattcttc tgcacgcagg tggcttgttt acgtatgttt ctggagccaa 61500
tttcctcggt gagatcattg aatggatcgg ctatgccctg gccacttggt ccctcccagc 61560
acttgcattt gcatttttct cactttgttt ccttgggctg cgagcttttc accaccatag 61620
gtaaattttt caataaaagc ggcagcattc acgtagcttt cttcttctcc aaacaggctt 61680
ttaacccgca gaggaagatt gagaaaccga agatatttaa ttttttaagg gaaggttgat 61740
actataatct gggttagcat attctgactt gctgggcttg tattgaagtt ggaagttagc 61800
tggatgagag tagcagtaat aaaatttttt ctaagaacaa acataagtcc atgtaaacag 61860
aggcaactga ggtgacggcc gggaaggtcc tgtgcctgtc ttgttgaaga aggctgtcca 61920
gcgagaagtg ccttgcacct tcttgggtta gctgacccag gctctgtgcc caccaggcag 61980
gcttacctgg agatgcttag ataaagcctc aagaagcgga agaagccgct tccatttcca 62040
ccttcagttt catcccctcc caccacattt ctggaagtgt gctccagagg tgggaccatg 62100
gccagcactt tccaaagctc cacagatatt tatttattta tttatttatt tatttatttt 62160
tgagttggag tctcactctg atgcccaggc tgaagtgcaa tggggcgatc ttgcctcact 62220
gcagccttca cctcccaggt tcaagtgatt ctcccacctc agccttccaa atggctgaga 62280
ctacaggccc accaccatgc ccagctaact ttttgcattt ttagtagaga caagtttcac 62340

catgttggcc aggctgtcct tgaactcctg acctcaagtg atctgcctgc ctcggcctcc 62400
caaagggctg ggattacagg caaagccatc acgcctggcc tccacagatg ttctgaggca 62460
cagcaggcta gagaaccact gggaaaaagt actatcttgg tgactatgtg gctgctattt 62520
ttggcaacaa gatttggtgc taacagttca ggtaatcaca gagccctgga actccagaag 62580
gattatttcc cctggaatct ctgcaatgcc agggtttatt ttggtactgc cttccttccc 62640
tgacacccac cctctataaa tcataaccaa ggccaaccct ggattctggg gaaggtagga 62700
caagaaatcc catgtatggg gcaatcttag gactgcccta tctgctggga aatgccaggg 62760
attgcaggtg tttcagaacc ctccctctga aggtctggcc taaagcttca ctaatccact 62820
aacctggggt ggagtgggga caaaagaatt aactaaaagt attgctggaa gtgaaaggta 62880
atatattagg ttgttatcag gctttaactt gccaagtgta aatgtcagat cctttcccta 62940
aaatggcttt tgtggaaaga gaaagcctat aattactgga gactatggat actcaaacag 63000
ggaatgagtg gtcttggaac caggaccctg gggttatgac tcaatgccta gttttgaaga 63060
tttaactaag aatgagttcc tttttttctg attagaattg ttcgaggaca acagttctga 63120
aatgaatgaa gcaacagcta gtgacctatt cctaccacct cctagactct gtgaggaggg 63180
gtggcagagg gttcctagcc cataaaagag tcataacagt tcttaccatt tcaggctggg 63240
tctgctgccc accagaggca gagcgggaat gggagaagag aaggcatcac tcagcacttg 63300
gagggtccct gggaaggagg gactctactg tgcttggtta ggggagggat ggtaattcca 63360
ccagacgttt ccagctgctg caacaacaaa acccaaattg aggcctcatc ctgtgatgtc 63420
agacctccca gagaagggcc agaaggcata gtttttaata ggctaacagg actttgtgaa 63480
ggcttctata aaacaaagcc aggcactcac atcagaggca gcacgggcgg aggcagccca 63540
ccagacttct caaatcacag taccgaaaac cagccacctt ttgtaactta ttatttgccc 63600
cctaattcaa actaaggtac tttaatacag tgtgtcatct tgattatgcc ttgaggaccg 63660
ccagcatcaa ctagttagga agacagcctg gcaacttaag cagacaggct tcttataaga 63720
tgcattcgtc tcctgtggct gctgcaatac attaccacaa actgggcggc ttaaaacaac 63780
acagatttgt cctttcatag ttctggaggc tagaattttg aaatcgaggc gtaggcaggg 63840
ccaggccccc gtgacggctc tagggaagaa ttcttccttg cctcttttta gcttctgatg 63900
gtggccggca acccttggtg ttccgtggct tatagctgca tcactctgat ctctgcctcc 63960
gtcttcacat ggccttctct cctgtgtgtc tctgtctcag tctctttgtc tcttctcctc 64020
ttctttttag gacacagtta tattggatta agggcacacc ctgctccatt atgacctcat 64080
cttaatttta tctgcaatgg tcctagtttc agaaaaaaaa aaattaccct ctcagttact 64140
gggggttagg acttcaacat atcttttgac gagacaaaat tcaacccatg atacatggtg 64200
acaatttgct ggcattccca ggcctcatga agggatattt tcctgggaac attgctggtt 64260

ctctttgccc atagtctttg gttccctgta tttcccagct gaatccaaac aagtacctcc 64320

ttctagatac tacatttttt tttctggtag gatatacgta acaaaaattt taccacttta 64380

gccgttttta attgtaaaat tcagtggcat taggtacatt cataatattg cacagccatc 64440

accactaccc tctgcctgtt acttttcatt tcccagcaaa agaagcttca acatttacaa 64500

gaaataggct gtgggaagga gaaataagaa tcataagtga ccatcgaaat agtcaggccc 64560

aaaataactg taggttgact tgtaacaaag atttggtaag agcaaacctc agctgtcagc 64620

cactgctcca ttatatttac aattattcct ttcttgtctt ttaggttcta cctcaagatg 64680

tttgaggact accccaaatc tcggaaagcc cttattccat tcatctttta aaggaaccaa 64740

attaaaaagg agcagagctc ccacaatgct gatgaaaact gtcaagctgc tgaaactgta 64800

attttcatga tataatagtc ccgtatatat gtaatagtag gtctcctggc gttctgccag 64860

ctggcctggg gattctgagt ggtgtctgct tagagtttac tcctaccctt ccagggaccc 64920

ctatcctgat ccccaactga agcttcaaaa agccactttt ccaaatggcg acagttgctt 64980

cttagctatt gctctgagaa agtacaaact tctcctatgt ctttcaccgg gcaatccaag 65040

tacatgtggc ttcataccca ctccctgtca atgcaggaca actctgtaat caagaatttt 65100

ttgacttgaa ggcagtactt atagacctta ttaaaggtat gcattttata catgtaacag 65160

agtagcagaa atttaaactc tgaagccaca aagacccaga gcaaacccac tcccaaatga 65220

aaaccccagt catggcttcc tttttcttgg ttaattagga aagatgagaa attattaggt 65280

agaccttgaa tacaggagcc ctctcctcat agtgctgaaa agatactgat gcattgacct 65340

catttcaaat ttgtgcagtg tcttagttga tgagtgcctc tgttttccag aagatttcac 65400

aatccccgga aaactggtat ggctattctt gaaggccagg ttttaataac cacaaacaaa 65460

aaggcatgaa cctgggtggc ttatgagaga gtagagaaca acatgaccct ggatggctac 65520

taagaggata gagaacagtt ttacaataga cattgcaaac tctcatgttt ttggaaacta 65580

gtggcaatat ccaaataatg agtagtgtaa aacaaagaga attaatgatg aggttacatg 65640

ctgcttgcct ccaccagatg tccacaacaa tatgaagtac agcagaagcc ccaagcaact 65700

ttcctttcct ggagcttctt ccttgtagtt ctcaggacct gttcaagaag gtgtctccta 65760

ggggcagcct gaatgcctcc ctcaaaggac ctgcaggcag agactgaaaa ttgcagacag 65820

aggggcacgt ctgggcagaa aacctgtttt gtttggctca gacatatagt tttttttttt 65880

tttacaaagt ttcaaaaact taaaaatcag gagattcctt cataaaactc tagcattcta 65940

gtttcattta aaaagttgga ggatctgaac atacagagcc cacatttcca caccagaact 66000

ggaactacgt agctagtaag catttgagtt tgcaaactct tgtgaagggg tcaccccagc 66060

atgagtgctg agatatggac tctctaagga aggggccgaa cgcttgtaat tggaatacat 66120

ggaaatattt gtcttctcag gcctatgttt gcggaatgca ttgtcaatat ttagcaaact 66180

gttttgacaa atgagcacca gtggtactaa gcacagaaac tcactatata agtcacatag 66240

gaaacttgaa aggtctgagg atgatgtaga ttactgaaaa atgcaaattg caatcatata 66300

aataagtgtt tttgttgttc attaaatacc tttaaatcat ggatgttaag cagttttgtt 66360

tgaattaaaa tatcctggga cttctggaga ttttcacaag gtattggggt gtgcttccct 66420

gtcccgcctg tccctcattc ccattcaccc tgtctgtagt gtcgtttcct ttcttctctt 66480

ctctcttcat gaaattaggg gctgtgtgct ggaaataaag aagtatgact tatacagcct 66540

ctcagccaca attcagaact acaaggaagt acaataaagg tgcaggaaaa cgtcatgagg 66600

ttagatgcca ctcctggtgc tgaggaatac acaggggaa tgaacacact tggtgaagta 66660

aatcttcagg tgtagcttga gctctgtgac ataaaagact tccagttctc tccatgacat 66720

tgaaaactac cttgcttaag tcctttattt tactaccatg taaaacatcc aggccggtcc 66780

ttgagatgaa ataaatatac aataaatggc agtactcagt ctcaggacaa aaccgccatt 66840

tggcaatttc acttttgcc acaagagggc gctttctaaa atagtattta gtccaacctt 66900

gacttaatta ggtccaaccc cagtcctgtt gcctgatcgt ggacctttca agttagcatg 66960

atcgtggaac ttcttaatct gaatataggg tagagtagcg tgaactctat gaaagctgaa 67020

accttccctt gataattcag gtattctcag tgttctaggg ctgttgtgtt caatgacagt 67080

ttgtcattgt ttagggctag gatatgtatg tggattaaat acagtaaagg tctgaacatg 67140

tgctcatctc taaacatatt tcttcccact tttaaaaata gggtgcaaca aaattatagt 67200

taattgaggt ttccatggac tgtttttgg ctaaaataat ctaacagtgt cctagctcac 67260

aagatactct atcttggtct tgctgaagct ttcacggaag aggcgttttc ctgccaacct 67320

tgaagaaaat gttgagtttt gtttgttttt cagaatttag acttaaagag ctgaagcaga 67380

cctcagacat cagctattcc taccacttca cattataggt agtgacactg agacccacag 67440

agttaaaagg cctcctcaca gctggtacag agctggtcag agcagccatc tcattttgtc 67500

cctttgaggg tcagatgtat gcttcttctg cttaaggcac agcctttagg gctgccatct 67560

ggatttctac agagctcatg caggagaaaa atagccagag cttaagtgct gttgcatagt 67620

tcagtttata cacctattgt cccatgcctg tttgtgtgtg aggcttccct cgctccgtgg 67680

gagcaccagg ctcatgccct ttcataaacc tatttgacag aatagagagt tttccctcat 67740

tggtgtagtc aagacaacat gtgtgttcag catggaaaaa aggtttcagg tcataaaccc 67800

ccttatccct aatgcttact ttcataaaga acaacagtgg ctccactgta ttctaaaagg 67860

aaaaaggagc tctaatgaga aatacgcaat taaacagcta tttaggcggc ttagaccctt 67920

tcaggaacaa ataaataaat ccgtggtttt acaaccctga agtttgataa tagctctctt 67980

ggatttttgt ggttacctca tggcaatctc actaagaagc aggggagcaa gctcttggca 68040

catgaaggaa taggctcatg aagattcatt tcttttcccg cttggccttt tggttctcta 68100

ataagctgtg agctgaggtc catgcaggga aaacaaggag ggtaacggca aatgtaaagt 68160

gaatttttct ggagaaggat gctgattatt ttatagcatc tacactatcc tatgatgaaa 68220

gaggcataga gccgggtggc aatgtgagtt cttgggtgat ttaataagcc atcgagtgga 68280

tttaatttct aagtaagaca tttgtttatt ctttgtacaa gtccatggag ttgtgatctt 68340

aaagagttct gtgttatttg cattgtgcct catttctccc catcaacctt agcttgagat 68400

ttggatgaat aaaataaata actggagaag gttaaagtat gcaccaagct gtgttagttt 68460

ctttagtcct gtctttttgg gttgagggtt tggttttgct caatgcagta acaatctaga 68520

ttctttattg gagggatagc gaatatccct tccgacatgg caagctggct gggaggagga 68580

ggacaacaga gaaagtggag gaaggagggg agtaatgagc gagggtctaa gggagggttg 68640

gcaatggaag gcccttgaga gagaggggcc tcccactgac agagtgggct tcctcccttt 68700

cctgtgtcca ggctgcacaa gcctggtccc ttctttatcc tcccaggaaa agacctccct 68760

ctgacagaga gaataaacac ttgttagagc tccatttcat aaaagaagaa gctgactttt 68820

aaaaaacaca agccatttgg ctgtgcttca ccataaataa ttgtatttct gtctgctcac 68880

ctcgtaaaga tagttttagt tctgcgtagt agtgacattg tgagaaagag gtgaagtaat 68940

tgctcttaga gcgtgtggca gcatccaagt cggctgaggc caatgggaag atgggagcat 69000

ccagaagaat aagcaactgc cagggttccc cttttcaagg cctttgtttt cctttactcc 69060

agacgcactc cccaaaaaag gatccttcct tatagagaag cgtttttaca gtgttgacta 69120

gaaagcaata ccgtaaaatc aattaaattt tgtcaatgta ttagtgcttt catttgttac 69180

aagttgcctt tcagatacta tttcattaaa ataattcttt atgatggttt ataacaggat 69240

aagctctgaa cagataagta agtgagggga agtagaaata ggagtaaaaa gtaaaataaa 69300

gccagagata aagttaaaat gcaaaaatgc ccttggaaga tcatgtacag tggctaaatc 69360

taaacataaa ttgggtcctg agtctccaaa gtacagaagg aaattaccag ttgctaaatc 69420

cacaacattc acaaaagaaa aacaacttga ccagggaaac acaactatta ccggtactga 69480

gactcatgat aaatttctac actgtgtgat gtggggaact atgttcatga gagcatcttt 69540

acaataaatg caggggtcac tttgtgcagc ttcttataat gtctttccac aaggacaaca 69600

ttctaatgcg cagctcaatt ctttagaagc aaaggggatg aggaggtttt ttttccactt 69660

agggtgtaga aagccaccag ataaccattc ctactctaaa aatgagaaaa aaccagatag 69720

tatataagat tataactttt tgagcctttt aatgaactga gataggagag caaccagaag 69780

aactgaattt cagaggaaac acacaaaccg tttcactttc agcggagtat gggaggaaga 69840

ggtaatggcc ataagagtgg gaaagaagaa aacaacagaa atttcaatga attatcaata 69900

gctgagtgga acctagcatg agattagaat ccctgggaga ctcagacact tggctgaaca 69960

agcatccaga tctgccccag gatgaggagt ttcctgggac acaggacttt ctgtgctcaa 70020

actggaaaag tcctaggcag accaggatga cctggtcacc ttagtctggt tgccaggtct 70080

tttacccaga cctccacctg gagcttatga ggtgggttgg ggacagggaa ggggatctga 70140

gagggccctt ctttggtggt gcatagttac aaaagcccac tgtattagtt cgttttcatg 70200

ctgctgataa agacatacct gaaactggga acaaaaagag gtttaattgg acttacagtt 70260

ccacatggct ggggaggcct cagaatcatg gctgtggaaa gagaaaaatg aggaaaaagc 70320

aaaagcggaa atccctgata aacccatcag atctcgtgag acttattcac tatcacgaga 70380

atagcatggg aaagaccagc ccccatgatt caattacctg cccctgggtc cctcctacaa 70440

catgtgggaa ttctgggaga tacaattcaa gttgagattt aggtggggac acagccaaac 70500

catatcatcc caccctggc ccctccaaat ctcatgtcct cacatttcaa aaccaatcat 70560

accttcccaa cagtccccca aagtgttaat tcatttcagc attaacccaa agtccacagt 70620

ccaaatactc atttgagaca aagcaagtcc cttctaccta ggagcctgta aaatcaaaag 70680

aaagctagtt acttcctaga tacaatgtgg gtacaggtat tcggtaaata cagccattct 70740

gaatgggaga aattggccaa aacaaagggg ttacagggcc catgcaagtc cagaatccag 70800

caggtcagtc aaatttaaa gctccaaaat gatctccgtt gactccaggt ctcgcatcca 70860

ggtaacgctg atgcaagagg tgggttccca tggtcttggg cagctccacc cctgtggctt 70920

tgcagggtac agcctccttt ccggctgact tcacgagctg gtgttgagta tctgtggctt 70980

ttccaggcac gtggtgcaag ctgttggtgg atctaaaatt ctgggatctg gagaacagtg 71040

gccctcttct cacagctcca ctaggcagtg ccccagtagg gactctgtgt gggtctttga 71100

ccccacattt cccttccaca ctgccctatc agaggttctc cataagagcc ctgcccctgc 71160

agcaaacttg cctgggcatc caggtgtttc catacatctt ctgaaatcta tgcagaggtt 71220

cccaaacctc agttcttggc ttctgtgcac ctgcaggctc aacatcacat ggaaggtgcc 71280

aaggcttgga gtttttaccc tctaaggcca cattctgagc tgtacattgg ccccctttcag 71340

ccatggttgg agcagctgga acacaggaca ccaagtccct aggctgcaca cagtgtaggg 71400

accctgggcc cagcccttga agccactttt tcctcctggg cctccaggcc tgtgatggga 71460

ggagctgctg tgaaggtctg tgacgtggcc tagagacatt ttccccatgg tcttggggat 71520

taacattagg ctccttgcta tttatgaaaa tttctacagc tggcttgaat atctccccag 71580

aaaatgggtt tttcttttct atcacattgt caggctgcaa attttctaaa cttttgtgct 71640

ctgcatcctt tgtaaaactg aatgccttta atagtaccca agtcatctct tgaatgcctt 71700

gttgcttaga aatttcttcc accagatatc ctaaatcatc tttctcaagt tccacaaatc 71760

tctaggacgg gggcaaaatg cctccagtct ctttgctaaa acataacaag agtcaccttt 71820

agtctagttc ccaataagtt tctcatctcc atctgagacc accccagcct ggaccttatt 71880

gtccacattg ctatcagcat tttgggcaaa gccattcaac aagtttttag gaggttccaa 71940

actttcccac attttcctgt cttcttctga gccctccaaa ctgttccaac ctctgcctgt 72000
tacccagttc caattccaca tttttgggta tcttttcagc aatgctccac tctactgcta 72060
ctaatttact gtatgagttc attttcacac tgctgataaa gacatacctg aaagtgggaa 72120
caaaaagagg tttaattgga cttacagtta tatatggcta gggaggcctc agaatcatgg 72180
tgggggggtga aaggcattcc ttacatggtg gtggcaagag acaaatgaga atatcactat 72240
cacgagaata gcacgggaaa gactggcccc catgattcaa ttacctcccc cgggtccctc 72300
acacagcacg tgggaattct gaaagataca attcaagttg agattcgggt ggggtcacag 72360
ccaaactata tcacccacct tcttccaggg ctttctgtta tagaaagcaa aacctgcaag 72420
cctctgggag agggatacga aaccctcctt ctctaagaca caggcaaagg tccactgact 72480
ctaggggagg ggataaagca aaaaagaacc agaaaagagg gcattcagga aactgcccca 72540
tcccctgcta tactgtcact gagaaagggg tagaaacaaa aactatttct tctaaggggg 72600
tgggtgggga gaaggcagca aatccagcaa ctctgaccaa gagccttgtt ccaaggagca 72660
agcattagca ggctactgca tggacatcgg gaaatggccc cagtctcagg caatgttaca 72720
ctgatgctga tggaggggta gatgcagaag ctgtctgtcc tcaaggaggg gagaggaaac 72780
ccaatctgga cagaagcctg cagagctaca aagaagaggt ctgcatcact acgggtccct 72840
cctgactaag actcccccac agtccagcat ttggctgcag agtgtgggat atggtgcagg 72900
aatgctgaga attccacacc atagtggccg agccccttag gactcaccta agactgaggc 72960
tggagtaggg gcgcctagga actatcctaa gtccagcata cacctcacac ccaatagtga 73020
gcaagagcaa agaagaaaag aagggaaatt tcaacaaatt atcaatagtt gagtggggcc 73080
tagcatgagt ttagaatccc tgggagcctc agatactcag ttgaccaagc acccagttct 73140
gccccagact gaggggtttc ctgggacaca ggactttcca tgcttaaact gcaaaagttc 73200
cccgcaaacc gggatgagtt ggtctctact gctggggagc acacagagag aaccacgcat 73260
gtggcacagg catgctgaga gctgagagta gagaagaaac aaggaatagc ccctctggcc 73320
ctccaggcct cacagtaagc acaaggcagc agcagctcat cgtggaaaga atctgaggag 73380
tgtgatgcat tacaagttaa ttcagtaaaa caaaccccaa atctagcctg ttcccccagc 73440
ccccaactta tgatctggta gaaaaggcaa gcttaattct gggtataaat actatttacc 73500
tcagtctcta ctgttccttt atgtttggcg ttgaataaaa agtatgaaca cacatacaca 73560
tacataaaac aaggcaaaaa acaaaaagat aatccactgt gacgagataa agcagtcaac 73620
agaatgagac aaagaagtgg tccagatatt agaactatca gatagggaca ttaaactaat 73680
tatcattaat atatagaagg atctagagga aaaggtggtg aacatgcatg agcagatgaa 73740
gaatgtcagc agaaagacaa aaactaaaca aattccaagg gaaatgctga caaatctccc 73800
cacaacatca agagataaag aattaatggg cttggcagcc tggatacagt aaaaaatcag 73860

taaacttgaa gacagatcaa tagatttatc caaactgaat caaagagaga aaaaaatatg 73920
tgtaattaga gtcccataag ggtggggtgg ggcagaaggg ggaggggaga gagagagaga 73980
gataaattga gacagaagat ttcttaagca aatgcataaa gagaaagcag acagttagtc 74040
ctcatctgga aaactgtgaa gtgggtgaaa tctaatgtga gcaaatgatt atcctctttc 74100
ttctggcatc atactttctg gtatgatgcc agaagaaaga ggttacctgt taaagaatat 74160
ccaaactatg ttagttgttg acagcacaag gtctgattgt atccagggga tatttgcatt 74220
tcactgaagg aacatttgca taaagatgga aggtcttcaa ggtccacatt aatgaattta 74280
tggtgaaata tccaccctct gcccagctaa tgggactaat ttgaggtcca taccttatct 74340
aagaccactc atacacatca ttcgaagtgg tactcacatt aaaccttcta ggatgaaggc 74400
tggacttta tacccattgt ttcagttgtg actcaaaggg gtccagccac agggcagaga 74460
ggggctggag ctgtgagcct gcttcctggg tcagtaattt tgtttctgtg ctctatgaga 74520
ctgatgcaca aacttggagg ctcaggactg tgacagtccc caacaccaga cagtctagca 74580
gagcacctag agccaggaac tttccctcca acagttgccc tatggttgtg cttttcaaag 74640
tattgtttct ggacccctcc atcagaattg ccaaggtgct cctattctgt ctgatctact 74700
ttgacattta gtcatgttct caccacactt tatcccacct tttcagagcc accactatct 74760
ctcagaattg tcataaaagt ttctcaactg atctccccac ttccatactt gcttccccat 74820
agtgtattct caacacagca agcagtcaga gtgatacttt tataagtact tgtaaacctt 74880
ttcgcatcat cttcaaaaca gtatttgggc tcccatctca cccagagcaa aagagtaagt 74940
ctttgcagtg gcctacaaag ctctacagaa tctgggctcc attacctctc tgactttatc 75000
tcctgttgct ctccatgtgg cccactgtcc actaccatgc tgacttcctg gaagatcctc 75060
aaaaccccct cagccctagg atctttgcac atgctcactc ctctgcctag aacgctcttc 75120
tttcagacac tcacgtggct cacctctcac ttccttcagg tgcctgctca aataccgcgt 75180
tgtaagaaag gtctttcctg cccatcctgt tcaacatagt gccccactcc taccttggt 75240
acactttctg ccttatccct ataatggttt tcaaagcact tacaccgtct aatacacaag 75300
acagttccta gtttatgtgt tcattctctg tctttcccca ctagactata agcccccgaa 75360
ggcaaggact tgtgtgtttt gtcctctgct gtgtcatcag tatttgcatg ggtgcctggc 75420
ataaaatgag agcttagtaa atatttatac tatgggaaga gctagaagca aattttcctt 75480
tctctaaatg tgggggtact tggagagaaa aggactccta aacatggcta aaacatgtac 75540
aaactttact gctgcttccc atcatcctga gacctgggag gaataaaaga aaggatggca 75600
agctgaatgg gattttaaag gctagatctt gccattctag gtaattaata catgactcct 75660
gctcatgata aagaaggtgg tggtgtttgc atcagtgtat ggatctctaa gggggctggg 75720
cctggtatca tccagtcaag catagagcag agtgtccagg caggtcctgg caggtgtggt 75780

ggaagattgg cagtggccac tggatgaggt gcatgtcctg atgcctcagg cagtcctgga 75840

cagacggtca tttggctcct tctttttggc ataggttggc cacttgtcaa gtgtggccag 75900

gccttcaggc tgggctgctc ggtcataagt aatacactaa cctggctggg cacggtggct 75960

catgcctgta atcccagcac tttgggaggc cgagaagggc ggatcacgag gtcaggagat 76020

caagaccatc ctggctaaca tggtgaaacc ccgtctctac taaagaaata caaaaaatta 76080

gccgggcatg gtagcgggcc cctgtagtcc cagctactgg cgaggctaag gcaggagaat 76140

ggtgtgaacc cgggaggcgg ggcttgcagt gagccgagat cgcaccactg cactccagcc 76200

tgggtgacag aacaagactc tatctcaaaa aaaaaaaaaa aaaaaatagt aatacactaa 76260

ccctttaaac acacacacac acacacaaac acacacacac aaacaagcac agttccacat 76320

ttcaactctc attctggtgc c 76341

<210> 42
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (101)..(101)
<223> Alternative allele: G.

<300>
<308> NCBI SNP CLUSTER ID: rs2687116
<309> 2003-03-07

<400> 42
cccttttgtgg aaaacaccaa gaagctttta agatttgatt ttttggatcc attctttctc 60

tcaataagta tgtggactac tatttccttt tatttatctt tctctcttaa aaataactgc 120

tttattgaga tataaatcac catgtaattc atccacttaa aatatacagt tcagtgattt 180

gtagtacatt tgaagatatg t 201

<210> 43
<211> 189
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (89)..(89)
<223> Alternative allele: T.

<300>
<308> NCBI SNP CLUSTER ID: rs1851426
<309> 2003-03-07

<400> 43
ttgggtgtgt ggcgggtgtg tccgcgtttt aaaaagcgcc gcacgctttg aactccaatt 60

ccacccccaa gaggctggga ccatcttact ggagtccttg atgctgtgtg acctgcagtg 120

accactgccc catcattgct ggctgaggtg gttggggtcc atctggctat ctgggcagct 180

gttctcttc 189

<210> 44
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (181)..(181)
<223> Alternative allele: A.

<300>
<308> NCBI SNP CLUSTER ID: rs676033
<309> 2003-03-07

<400> 44
actattctcc tgccctaatc agccaggtcc aggtaacaga aaagtaaaga cagccgctgt 60

accccagagc ctgctaaaag tattcaaacg agctaatcct aagcctgatt accttgtcat 120

gcccactctt tcctgcagaa actacagtaa aggctcttgc ccaccttgac ccctcactcc 180

ggctgcctcc taacactggt gcttctccat gtggtcttgg gtggtgtgct gtgtcttctg 240

tttgtaggga tctgtcgata taaacctttt ccttcacgat a 281

<210> 45
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> SNP
<222> (81)..(81)
<223> Alternative allele: A.

<300>
<308> NCBI SNP CLUSTER ID: rs1042578
<309> 2003-03-07

<400> 45
ggtactaagc acagaaactc actatataag tcacatagga aacttgaaag gtctgaggat 60

gatgtagatt actgaaaaat gcaaattgca atcatataaa taagtgtttt tgttgttcat 120

taaatacctt taaatcatgg atgtaagcag tttgttgata 160